

## Sequence Table

(2) INFORMATION FOR SEQ ID NO: 1:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

10 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

15 (D) CLONE NAME: HP01263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

20	1	5	10	15
	Met Gly Leu Leu Leu Pro Leu Ala Leu Cys Ile Leu Val Leu Cys Cys			
	Gly Ala Met Ser Pro Pro Gln Leu Ala Leu Asn Pro Ser Ala Leu Leu			
	20	25	30	
	Ser Arg Gly Cys Asn Asp Ser Asp Val Leu Ala Val Ala Gly Phe Ala			
	35	40	45	
25	Leu Arg Asp Ile Asn Lys Asp Arg Lys Asp Gly Tyr Val Leu Arg Leu			
	50	55	60	
	Asn Arg Val Asn Asp Ala Gln Glu Tyr Arg Arg Gly Gly Leu Gly Ser			
	65	70	75	80
	Leu Phe Tyr Leu Thr Leu Asp Val Leu Glu Thr Asp Cys His Val Leu			
30	85	90	95	
	Arg Lys Lys Ala Trp Gln Asp Cys Gly Met Arg Ile Phe Phe Glu Ser			
	100	105	110	
	Val Tyr Gly Gln Cys Lys Ala Ile Phe Tyr Met Asn Asn Pro Ser Arg			
	115	120	125	
35	Val Leu Tyr Leu Ala Ala Tyr Asn Cys Thr Leu Arg Pro Val Ser Lys			
	130	135	140	
	Lys Lys Ile Tyr Met Thr Cys Pro Asp Cys Pro Ser Ser Ile Pro Thr			
	145	150	155	160

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      Asp Ser Ser Asn His Gln Val Leu Glu Ala Ala Thr Glu Ser Leu Ala
                165                      170                      175
      Lys Tyr Asn Asn Glu Asn Thr Ser Lys Gln Tyr Ser Leu Phe Lys Val
                180                      185                      190
5   Thr Arg Ala Ser Ser Gln Trp Val Val Gly Pro Ser Tyr Phe Val Glu
                195                      200                      205
      Tyr Leu Ile Lys Glu Ser Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys
                210                      215                      220
      Ser Leu Gln Ser Ser Asp Ser Val Pro Val Gly Leu Cys Lys Gly Ser
10  225                      230                      235                      240
      Leu Thr Arg Thr His Trp Glu Lys Phe Val Ser Val Thr Cys Asp Phe
                245                      250                      255
      Phe Glu Ser Gln Ala Pro Ala Thr Gly Ser Glu Asn Ser Ala Val Asn
                260                      265                      270
15  Gln Lys Pro Thr Asn Leu Pro Lys Val Glu Glu Ser Gln Gln Lys Asn
                275                      280                      285
      Thr Pro Pro Thr Asp Ser Pro Ser Lys Ala Gly Pro Arg Gly Ser Val
                290                      295                      300
      Gln Tyr Leu Pro Asp Leu Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro
20  305                      310                      315                      320
      Gln Glu Ala Phe Pro Val His Leu Asp Leu Thr Thr Asn Pro Gln Gly
                325                      330                      335
      Glu Thr Leu Asp Ile Ser Phe Leu Phe Leu Glu Pro Met Glu Glu Lys
                340                      345                      350
25  Leu Val Val Leu Pro Phe Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys
                355                      360                      365
      Pro Gly Pro Ala Gln Asn Ala Ser Pro Leu Val Leu Pro Pro
                370                      375                      380

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30

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317

(B) TYPE: Amino acid

35

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP01299

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Met Trp Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His
  1             5             10             15
10 Trp Tyr Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val
      20             25             30
Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln
      35             40             45
Leu Asp Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys
15      50             55             60
Gly Ala Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val
      65             70             75             80
Thr Leu Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp
      85             90             95
20 Val Lys Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn
      100            105            110
Ala Gly Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu
      115            120            125
Asp Ser Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val
25      130            135            140
Thr Leu Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val
      145            150            155            160
Asn Val Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr
      165            170            175
30 Cys Val Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg
      180            185            190
Glu Ile Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr
      195            200            205
Phe Arg Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys
35      210            215            220
Gln Ser Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln
      225            230            235            240
Gln Tyr Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn

```

245 250 255  
 Cys Ser Thr Asn Leu Asn Leu Val Thr Asp Cys Met Glu His Ala Leu  
 260 265 270  
 Thr Ser Val His Pro Arg Thr Arg Tyr Ser Ala Gly Trp Asp Ala Lys'  
 5 275 280 285  
 Phe Phe Phe Ile Pro Leu Ser Tyr Leu Pro Thr Ser Leu Ala Asp Tyr  
 290 295 300  
 Ile Leu Thr Arg Ser Trp Pro Lys Pro Ala Gln Ala Val  
 305 310 315  
 10

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296  
 15 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: Protein  
 (iii) HYPOTHETICAL: No

## 20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Liver  
 (D) CLONE NAME: HP01347

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ser Asp Ser Lys Glu Pro Arg Val Gln Gln Leu Gly Leu Leu Gly  
 1 5 10 15  
 Cys Leu Gly His Gly Ala Leu Val Leu Gln Leu Leu Ser Phe Met Leu  
 20 25 30  
 Leu Ala Gly Val Leu Val Ala Ile Leu Val Gln Val Ser Lys Val Pro  
 35 40 45  
 Ser Ser Leu Ser Gln Glu Gln Ser Glu Gln Asp Ala Ile Tyr Gln Asn  
 50 55 60  
 35 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys  
 65 70 75 80  
 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly  
 85 90 95

Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr  
                     100                    105                    110  
 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln,  
                     115                    120                    125  
 5 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu  
                     130                    135                    140  
 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu  
                     145                    150                    155                    160  
 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile  
 10                    165                    170                    175  
 Tyr Gln Glu Leu Thr Glu Leu Lys Ala Ala Val Gly Glu Leu Pro Glu  
                     180                    185                    190  
 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala  
                     195                    200                    205  
 15 Ala Val Gly Glu Leu Pro Asp Gln Ser Lys Gln Gln Gln Ile Tyr Gln  
                     210                    215                    220  
 Glu Leu Thr Asp Leu Lys Thr Ala Phe Glu Arg Leu Cys Arg His Cys  
                     225                    230                    235                    240  
 Pro Lys Asp Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn  
 20                    245                    250                    255  
 Ser Gln Arg Asn Trp His Asp Ser Val Thr Ala Cys Gln Glu Val Arg  
                     260                    265                    270  
 Ala Gln Leu Val Val Ile Lys Thr Ala Glu Glu Gln Leu Pro Ala Val  
                     275                    280                    285  
 25 Leu Glu Gln Trp Arg Thr Gln Gln  
                     290                    295

## (2) INFORMATION FOR SEQ ID NO: 4:

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

## 35 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

5  
 Met Cys Thr Gly Lys Cys Ala Arg Cys Val Gly Leu Ser Leu Ile Thr  
 1 5 10 15  
 Leu Cys Leu Val Cys Ile Val Ala Asn Ala Leu Leu Leu Val Pro Asn  
 20 25 30  
 10 Gly Glu Thr Ser Trp Thr Asn Thr Asn His Leu Ser Leu Gln Val Trp  
 35 40 45  
 Leu Met Gly Gly Phe Ile Gly Gly Gly Leu Met Val Leu Cys Pro Gly  
 50 55 60  
 Ile Ala Ala Val Arg Ala Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys  
 15 65 70 75 80  
 Cys Gly Asn Arg Cys Arg Met Leu Arg Ser Val Phe Ser Ser Ala Phe  
 85 90 95  
 Gly Val Leu Gly Ala Ile Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu  
 100 105 110  
 20 Arg Asn Gly Pro Arg Cys Leu Met Asn Gly Glu Trp Gly Tyr His Phe  
 115 120 125  
 Glu Asp Thr Ala Gly Ala Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg  
 130 135 140  
 Cys Glu Ala Pro Pro Arg Val Val Pro Trp Asn Val Thr Leu Phe Ser  
 25 145 150 155 160  
 Leu Leu Val Ala Ala Ser Cys Leu Glu Ile Val Leu Cys Gly Ile Gln  
 165 170 175  
 Leu Val Asn Ala Thr Ile Gly Val Phe Cys Gly Asp Cys Arg Lys Lys  
 180 185 190  
 30 Gln Asp Thr Pro His  
 195

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 221  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 5 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP01526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

10 Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
    1           5           10           15
Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
    20           25           30
Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe Leu
15    35           40           45
Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
    50           55           60
Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
    65           70           75           80
20 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
    85           90           95
Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
    100          105          110
Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
25    115          120          125
Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
    130          135          140
Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
    145          150          155          160
30 Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
    165          170          175
Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
    180          185          190
Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
35    195          200          205
Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
    210          215          220

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## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251

(B) TYPE: Amino acid

5 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

15

Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala Ile Thr Arg  
 1 5 10 15  
 Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys Leu Gly  
 20 25 30  
 Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala Phe Leu Tyr  
 35 40 45  
 Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr Phe Pro Val  
 50 55 60  
 Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr Phe Leu Tyr  
 25 65 70 75 80  
 Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly Arg Pro Ala  
 85 90 95  
 Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile Val Ile Thr  
 100 105 110  
 Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu Ile Met Ser  
 115 120 125  
 Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile Val Ser Phe  
 130 135 140  
 Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu  
 35 145 150 155 160  
 Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly  
 165 170 175  
 Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met



180 185 190  
 Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg  
 195 200 205  
 Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro  
 5 210 215 220  
 Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Gly Arg His  
 225 230 235 240  
 Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln  
 245 250

10

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106

15 (B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

(D) CLONE NAME: HP10389

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro Ser  
 1 5 10 15  
 30 Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn Pro  
 20 25 30  
 Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro Val  
 35 40 45  
 Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly Leu  
 35 50 55 60  
 Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met Arg  
 65 70 75 80  
 Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu Gly

85 90 95  
 Leu Ala Val Thr Ala Met Lys Ser Arg Pro  
 100 105

5

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: Protein  
 (iii) HYPOTHETICAL: No

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10408

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser  
 1 5 10 15  
 Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu  
 25 20 25 30  
 Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu  
 35 40 45  
 Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr  
 50 55 60  
 30 Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO: 9:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

10

Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly  
 1 5 10 15  
 Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly  
 20 25 30  
 15 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala  
 35 40 45  
 Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro  
 50 55 60  
 Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala  
 20 65 70 75 80  
 Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val  
 85 90 95  
 Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His  
 100 105 110  
 25 Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys  
 115 120 125  
 Gln Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu  
 130 135 140  
 Arg Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu  
 30 145 150 155 160  
 Glu Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys  
 165 170 175  
 Ala Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu  
 180 185 190  
 35 Lys Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr  
 195 200 205  
 Glu Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys  
 210 215 220

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino acid

20 (ii) SEQUENCE KIND: Protein

(vi) ORIGINAL SOURCE:

25 (B) CELL KIND: Stomach cancer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

30 Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
    1             5             10             15
    Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
        20             25             30
    Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
35             35             40             45
    Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp Asp Glu Pro Pro Pro
        50             55             60
    Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg

```

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino acid

25 (ii) SEQUENCE KIND: Protein

(vi) ORIGINAL SOURCE:

30 (B) CELL KIND: Stomach cancer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

1                      5                      10                      15

20                      25                      30

	Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile	
	35	40 45
	Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu His Glu Arg	
	50	55 60
5	Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser	
	65	70 75 80
	Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro Asn Lys Thr	
	85	90 95
	Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg Tyr Gln Ser	
10	100	105 110
	Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys Leu Tyr Glu	
	115	120 125
	Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu Leu Leu Lys	
	130	135 140
15	Leu Ser Glu Glu Leu Leu Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln	
	145	150 155 160
	His Val Pro Leu Ser Gln His Met Leu Gly Phe Ala Met Lys Ser Val	
	165	170 175
	Thr Gln Met Val Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile	
20	180	185 190
	Arg Phe Gln Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly	
	195	200 205
	Phe Leu Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr	
	210	215 220
25	Glu Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys	
	225	230 235 240
	Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser Leu	
	245	250 255
	Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser Met Ile	
30	260	265 270
	Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys Thr Trp Ala	
	275	280 285
	Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys Lys Leu Tyr Glu	
	290	295 300
35	Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val Thr Pro Glu Lys Ile	
	305	310 315 320
	Glu Gln Leu Arg Tyr Cys Gln His Val Leu Cys Glu Thr Val Arg Thr	
	325	330 335

Ala Lys Leu Thr Pro Val Ser Ala Gln Leu Gln Asp Ile Glu Gly Lys  
                   340                  345                  350  
 Ile Asp Arg Phe Ile Ile Pro Arg Glu Thr Leu Val Leu Tyr Ala Leu  
                   355                  360                  365  
 5 Gly Val Val Leu Gln Asp Pro Asn Thr Trp Pro Ser Pro His Lys Phe  
                   370                  375                  380  
 Asp Pro Asp Arg Phe Asp Asp Glu Leu Val Met Lys Thr Phe Ser Ser  
 385                  390                  395                  400  
 Leu Gly Phe Ser Gly Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr  
 10                  405                  410                  415  
 Met Val Thr Thr Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu  
                   420                  425                  430  
 Leu Ser Val Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr  
                   435                  440                  445  
 15 Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
                   450                  455                  460

## (2) INFORMATION FOR SEQ ID NO: 12:

## 20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: Protein

## 25 (iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer

## 30 (D) CLONE NAME: HP10419

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro  
 35 1                  5                  10                  15  
 Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val  
                   20                  25                  30  
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu

	35		40		45
	Ala	Ser	Val	Val	Trp
	50		55		60
	Ala	Arg	Leu	Gln	Tyr
5	65		70		75
	Leu	Leu	Gln	Glu	Val
	85		90		95
	Ala	Asp	Glu	Gly	Leu
	100		105		110
10	Ser	Ile	Arg	Gln	Met
	115		120		125
	Ser	Gly	Val	Phe	Ser
	130		135		140
	Gly	Val	Val	Gly	Ile
15	145		150		155
	Ala	Phe	Leu	Thr	Ala
	165		170		175
	Val	Phe	Phe	Asp	Ala
	180		185		190
20	Val	Val	Gly	Ser	His
	195		200		205
	Trp	Tyr	Glu	Ala	Ser
	210		215		220
	Gly	Leu	Trp	Ala	Phe
25	225		230		235
	Arg	Ser	Leu	Leu	Cys
	245				

30 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

35 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:



(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10424

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
  1             5             10             15
Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
10             20             25             30
Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
             35             40             45
Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
             50             55             60
15 Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
             65             70             75             80
Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
             85             90             95
Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
20             100             105             110
Thr

```

(2) INFORMATION FOR SEQ ID NO: 14:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

30 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Epidermoid carcinoma  
 (C) CELL LINE: KB  
 (D) CLONE NAME: HP10428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu  
 1 5 10 15  
 Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr  
 20 25 30  
 5 Phe Tyr Asn Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met  
 35 40 45  
 Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg  
 50 55 60  
 Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser Trp  
 10 65 70 75 80  
 Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala Leu  
 85 90 95  
 Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser Leu  
 100 105 110  
 15 Tyr Thr Met Thr Lys Ser Ser Ala Val Leu Phe Ile Leu Ile Phe Ser  
 115 120 125  
 Leu Ile Phe Lys Leu Glu Glu Leu Arg Ala Ala Leu Val Leu Val Val  
 130 135 140  
 Leu Leu Ile Ala Gly Gly Leu Phe Met Phe Thr Tyr Lys Ser Thr Gln  
 20 145 150 155 160  
 Phe Asn Val Glu Gly Phe Ala Leu Val Leu Gly Ala Ser Phe Ile Gly  
 165 170 175  
 Gly Ile Arg Trp Thr Leu Thr Gln Met Leu Leu Gln Lys Ala Glu Leu  
 180 185 190  
 25 Gly Leu Gln Asn Pro Ile Asp Thr Met Phe His Leu Gln Pro Leu Met  
 195 200 205  
 Phe Leu Gly Leu Phe Pro Leu Phe Ala Val Phe Glu Gly Leu His Leu  
 210 215 220  
 Ser Thr Ser Glu Lys Ile Phe Arg Phe Gln Asp Thr Gly Leu Leu Leu  
 30 225 230 235 240  
 Arg Val Leu Gly Ser Leu Phe Leu Gly Gly Ile Leu Ala Phe Gly Leu  
 245 250 255  
 Gly Phe Ser Glu Phe Leu Leu Val Ser Arg Thr Ser Ser Leu Thr Leu  
 260 265 270  
 35 Ser Ile Ala Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala  
 275 280 285  
 His Leu Leu Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala  
 290 295 300

Leu Cys Leu Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His  
 305                                      310                                      315                                      320  
 Ser Arg Gly Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser  
    325                                      330                                      335  
 5 Pro Asp Leu Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp  
    340                                      345                                      350  
 Asn Glu Glu Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln  
    355                                      360                                      365

10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226

(B) TYPE: Amino acid

15

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

25

Met Pro Thr Thr Lys Lys Thr Leu Met Phe Leu Ser Ser Phe Phe Thr  
    1                                      5                                      10                                      15  
 Ser Leu Gly Ser Phe Ile Val Ile Cys Ser Ile Leu Gly Thr Gln Ala  
    20                                      25                                      30  
 30 Trp Ile Thr Ser Thr Ile Ala Val Arg Asp Ser Ala Ser Asn Gly Ser  
    35                                      40                                      45  
 Ile Phe Ile Thr Tyr Gly Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu  
    50                                      55                                      60  
 Ser His Gly Leu Ala Glu Pro Lys Lys Lys Phe Ala Val Leu Glu Ile  
 35    65                                      70                                      75                                      80  
 Leu Asn Asn Ser Ser Gln Lys Thr Leu His Ser Val Thr Ile Leu Phe  
    85                                      90                                      95  
 Leu Val Leu Ser Leu Ile Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

30 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

35 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly  
1 5 10 15  
Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly  
20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys  
           35                          40                          45  
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys  
           50                          55                          60  
 5 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro  
      65                          70                          75                          80  
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser  
                           85                          90                          95  
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr  
 10                          100                          105                          110  
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile  
           115                          120                          125  
 Gln

15

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163

20 (B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP10433

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly Ala Val Gly  
      1                          5                          10                          15  
 Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly Leu Gln Val  
 35                          20                          25                          30  
 Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala Phe Gln  
           35                          40                          45  
 Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro Ala Gly Ile

50                      55                      60  
 Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys Arg Lys Arg  
 65                      70                      75                      80  
 Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg  
 5                      85                      90                      95  
 Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly  
 100                      105                      110  
 Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu  
 115                      120                      125  
 10 Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala Gly Glu Asp  
 130                      135                      140  
 Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser Lys Ala Leu  
 145                      150                      155                      160  
 Pro Arg Ser

15

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193

20 (B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10480

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro  
 1                      5                      10                      15  
 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly  
 20                      25                      30  
 35 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser S r Leu Trp  
 35                      40                      45  
 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly

	50		55		60											
	Cys	Gln	Ser	Leu	Met	Glu	Tyr	Ala	Trp	Gly	Arg	Ala	Ala	Ala	Ala	Met
	65			70					75							80
	Leu	Phe	Cys	Gly	Phe	Ile	Ile	Leu	Val	Ile	Cys	Phe	Ile	Leu	Ser	Phe'
5				85					90						95	
	Phe	Ala	Leu	Cys	Gly	Pro	Gln	Met	Leu	Val	Phe	Leu	Arg	Val	Ile	Gly
				100					105						110	
	Gly	Leu	Leu	Ala	Leu	Ala	Ala	Val	Phe	Gln	Ile	Ile	Ser	Leu	Val	Ile
				115					120						125	
10	Tyr	Pro	Val	Lys	Tyr	Thr	Gln	Thr	Phe	Thr	Leu	His	Ala	Asn	Arg	Ala
				130					135						140	
	Val	Thr	Tyr	Ile	Tyr	Asn	Trp	Ala	Tyr	Gly	Phe	Gly	Trp	Ala	Ala	Thr
	145				150					155						160
	Ile	Ile	Leu	Ile	Gly	Cys	Ala	Phe	Phe	Phe	Cys	Cys	Leu	Pro	Asn	Tyr
15				165						170					175	
	Glu	Asp	Asp	Leu	Leu	Gly	Asn	Ala	Lys	Pro	Arg	Tyr	Phe	Tyr	Thr	Ser
				180					185						190	
	Ala															

20

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146

(B) TYPE: Nucleic acid

25

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Linear

(D) CLONE NAME: HP01263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

35

ATGGGTCTGC	TCCTTCCCCT	GGCACTCTGC	ATCCTAGTCC	TGTGCTGCGG	ACCAATGTCT	60
CCACCCAGC	TGGCCCTCAA	CCCCTCGGCT	CTGCTCTCCC	GGGGCTGCAA	TGACTCCGAT	120
GTGCTGGCAG	TTGCAGGCTT	TGCCCTGCGG	GATATTAACA	AAGACAGAAA	GGATGGCTAT	180

	GTGCTGAGAC TCAACCGAGT GAACGACGCC CAGGAATACA GACGGGGTGG CCTGGGATCT	240
	CTGTTCTATC TTACTGGA TGTGCTAGAG ACTGACTGCC ATGTGCTCAG AAAGAAGGCA	300
	TGGCAAGACT GTGGAATGAG GATATTTTTT GAATCAGTTT ATGGTCAATG CAAAGCAATA	360
	TTTTATATGA ACAACCCAAG TAGAGTTCTC TATTTAGCTG CTTATAACTG TACTCTTCGC	420
5	CCAGTTTCAA AAAAAAAGAT TTACATGACG TGCCCTGACT GCCCAAGCTC CATACCCACT	480
	GACTCTTCCA ATCACCAAGT GCTGGAGGCT GCCACCGAGT CTCTTGCGAA ATACAACAAT	540
	GAGAACACAT CCAAGCAGTA TTCTCTCTC AAAGTCACCA GGGCTTCTAG CCAGTGGGTG	600
	GTCGGCCCTT CTTACTTTGT GGAATACTTA ATTAAAGAAT CACCATGTAC TAAATCCCAG	660
	GCCAGCAGCT GTTCACTTCA GTCCTCCGAC TCTGTGCCTG TTGGTCTTTG CAAAGGTTCT	720
10	CTGACTCGAA CACTGCGGA AAAGTTTGTC TCTGTGACTT GTGACTTCTT TGAATCACAG	780
	GCTCCAGCCA CTGGAAGTGA AAAGTCTGCT GTTAACCAGA AACCTACAAA CCTTCCAAG	840
	GTGGAAGAAT CCCAGCAGAA AAACACCCCC CCAACAGACT CCCCCTCAA AGCTGGGCCA	900
	AGAGGATCTG TCCAATATCT TCCTGACTTG GATGATAAAA ATTCCCAGGA AAAGGGCCCT	960
	CAGGAGGCCT TTCCTGTGCA TCTGGACCTA ACCACGAATC CCCAGGGAGA AACCTGGAT	1020
15	ATTTCTTCC TCTTCTGGA GCCTATGGAG GAGAAGCTGG TTGTCCTGCC TTTCCCCAAA	1080
	GAAAAAGCAC GCACTGCTGA GTGCCAGGG CCAGCCCAGA ATGCCAGCCC TCTTGTCTT	1140
	CCGCCA	1146

20 (2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 951

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

30 (B) CELL KIND: Liver

(D) CLONE NAME: HP01299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

35	ATGTGGCTCT ACCTGGCGGC CTTCGTGGGC CTGTACTACC TTCTGCACTG GTACCGGGAG	60
	AGGCAGGTGG TGAGCCACCT CCAAGACAAG TATGTCTTTA TCACGGGCTG TGAAGCGGGC	120
	TTTGGGAACC TGCTGGCCAG ACAGCTGGAT GCACGAGGCT TGAGAGTGCT GGCTGCGTGT	180
	CTGACGGAGA AGGGGGCCGA GCAGCTGAGG GGCCAGACGT CTGACAGGCT GGAGACGGTG	240



ACCCTGGATG TTACCAAGAT GGAGAGCATC GCTGCAGCTA CTCAGTGGGT GAAGGAGCAT 300  
 GTGGGGGACA GAGGACTCTG GGGACTGGTG AACAAATGCAG GCATTCTTAC ACCAATTACC 360  
 TTATGTGAGT GGCTGAACAC TGAGGACTCT ATGAATATGC TCAAAGTGAA CCTCATTGGT 420  
 GTGATCCAGG TGACCTTGAG CATGCTTCCT TTGGTGAGGA GAGCACGGGG AAGAATTGTC 480  
 5 AATGTCTCCA GCATTCTGGG AAGAGTTGCT TTCTTTGTAG GAGGCTACTG TGTCTCCAAG 540  
 TATGGAGTGG AAGCCTTTTC AGATATTCTG AGGCGTGAGA TTCAACATTT TGGGGTGAAA 600  
 ATCAGCATAG TTGAACCTGG CTAATTCAGA ACGGGAATGA CAAACATGAC ACAGTCCTTA 660  
 GAGCGAATGA AGCAAAGTTG GAAAGAAGCC CCCAAGCATA TTAAGGAGAC CTATGGACAG 720  
 CAGTATTTTG ATGCCCTTTA CAATATCATG AAGGAAGGGC TGTGAATTG TAGCACAAAC 780  
 10 CTGAACCTGG TCACTGACTG CATGGAACAT GCTCTGACAT CGGTGCATCC GCGAACTCGA 840  
 TATTCAGCTG GCTGGGATGC TAAATTTTTC TTCATCCCTC TATCTTATTT ACCTACATCA 900  
 CTGGCAGACT ACATTTTGAC TAGATCTTGG CCCAAACCAG CCCAGGCAGT C 951

15 (2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP01347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

30 ATGAGTGACT CCAAGGAACC AAGGGTGCAG CAGCTGGGCC TCCTGGGGTG TCTTGCCAT 60  
 GGC GCCCTG TGCTGCAACT CCTCTCCTTC ATGCTCTTGG CTGGGGTCTT GGTGGCCATC 120  
 CTTGTCCAAG TGTCCAAGGT CCCAGCTCC CTAAGTCAGG AACAAATCCGA GCAAGACGCA 180  
 ATCTACCAGA ACCTGACCCA GCTTAAAGCT GCAGTGGGTG AGCTCTCAGA GAAATCCAAG 240  
 CTGCAGGAGA TCTACCAGGA GCTGACCCAG CTGAAGGCTG CAGTGGGTGA GTTGCCAGAG 300  
 35 AAATCCAAGC TGCAGGAGAT CTACCAGGAG CTGACCCGGC TGAAGGCTGC AGTGGGTGAG 360  
 TTGCCAGAGA AATCCAAGCT GCAGGAGATC TACCAGGAGC TGACCCGGCT GAAGGCTGCA 420  
 GTGGGTGAGT TGCCAGAGAA ATCCAAGCTG CAGGAGATCT ACCAGGAGCT GACCCGGCTG 480  
 AAGGCTGCAG TGGGTGAGTT GCCAGAGAAA TCCAAGCTGC AGGAGATCTA CCAGGAGCTG 540

ACGGAGCTGA AGGCTGCAGT GGGTGAGTTG CCAGAGAAAT CCAAGCTGCA GGAGATCTAC 600  
 CAGGAGCTGA CCCAGCTGAA GGCTGCAGTG GGTGAGTTGC CAGACCAGTC CAAGCAGCAG 660  
 CAAATCTATC AAGAACTGAC CGATTTGAAG ACTGCATTG AACGCCTGTG CCGCCACTGT 720  
 CCCAAGGACT GGACATTCTT CCAAGGAAAC TGTTACTTCA TGTCTAACTC CCAGCGGAAC 780  
 5 TGGCAGGACT CCGTCACCGC CTGCCAGGAA GTGAGGGCCC AGCTCGTCGT AATCAAAACT 840  
 GCTGAGGAGC AGCTTCCAGC GGTACTGGAA CAGTGGAGAA CCCAACAA 888

## (2) INFORMATION FOR SEQ ID NO: 22:

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 15 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 20 (D) CLONE NAME: HP01440

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ATGTGTACGG GAAAATGTGC CCGCTGTGTG GGGCTCTCCC TCATTACCCT CTGCCTCGTC 60  
 25 TGCATTGTGG CCAACGCCCT CCTGCTGGTA CCTAATGGGG AGACCTCCTG GACCAACACC 120  
 AACCATCTCA GCTTGCAAGT CTGGCTCATG GCGGCTTCA TTGGCGGGGG CCTAATGGTA 180  
 CTGTGTCCGG GGATTGCAGC CGTTCGGGCA GGGGGCAAGG GCTGCTGTGG TGCTGGGTGC 240  
 TGTGGAACC GCTGCAGGAT GCTGCGCTCG GTCTTCTCCT CGGCGTTCGG GGTGCTTGGT 300  
 GCCATCTACT GCCTCTCGGT GTCTGGAGCT GGGCTCCGAA ATGGACCCAG ATGCTTAATG 360  
 30 AACGGCGAGT GGGGCTACCA CTTGAAGAC ACCGCGGGAG CTTACTTGCT CAACCGCACT 420  
 CTATGGGATC GGTGCGAGGC GCCCCCTCGC GTGGTCCCCT GGAATGTGAC GCTCTTCTCG 480  
 CTGCTGGTGG CCGCCTCCTG CCTGGAGATA GTACTGTGTG GGATCCAGCT GGTGAACGCG 540  
 ACCATTGGTG TCTTCTGCGG CGATTGCAGG AAAAAACAGG ACACCCCTCA C 591

35

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: cDNA to mRNA

5

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP01526

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

	ATGGAGGCGG GCGGCTTTCT GGA	CTCGCTC ATTTACGGAG CATGCGTGGT	CTTCACCCTT	60
	GGCATGTTCT CCGCCGGCCT CTCGGACCTC	AGGCACATGC GAATGACCCG GAGTGTGGAC		120
15	AACGTCCAGT TCCTGCCCTT TCTCACCACG	GAAGTCAACA ACCTGGGCTG GCTGAGTTAT		180
	GGGGCTTTGA AGGGAGACGG GATCCTCATC	GTGCTCAACA CAGTGGGTGC TGC	GCTTCAG	240
	ACCCTGTATA TCTTGGCATA TCTGCATTAC	TGCCCTCGGA AGCGTGTGT GCTCCTACAG		300
	ACTGCAACCC TGCTAGGGGT CTTTCTCCTG	GGTTATGGCT ACTTTTGGCT CCTGGTACCC		360
	AACCCTGAGG CCCGGCTTCA GCAGTTGGGC	CTCTTCTGCA GTGTCTTCAC CATCAGCATG		420
20	TACCTCTCAC CACTGGCTGA CTTGGCTAAG	GTGATTCAAA CTAAATCAAC CCAATGTCTC		480
	TCCTACCCAC TCACCATTCG TACCCTTCTC	ACCTCTGCCT CCTGGTGCCT CTATGGGTTT		540
	CGACTCAGAG ATCCCTATAT CATGGTGTCC	AACTTTCCAG GAATCGTCAC CAGCTTTATC		600
	CGCTTCTGGC TTTTCTGGAA GTACCCCCAG	GAGCAAGACA GGA	ACTACTG GCTCCTGCAA	660
	ACC			663

25

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 753

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

      ATGTCGGACA TCGGAGACTG GTTCAGGAGC ATCCCGGCGA TCACGCGCTA TTGGTTCGCC      60
      GCCACCGTCG CCGTGCCCTT GGTGGGCAAA CTCGGCCTCA TCAGCCCGGC CTACCTCTTC      120
5    CTCTGGCCCG AAGCCTTCCT TTATCGCTTT CAGATTGGA GGCCAATCAC TGCCACCTTT      180
      TATTTCCCTG TGGGTCCAGG AACTGGATTT CTTTATTTGG TCAATTTATA TTTCTTATAT      240
      CAGTATTCTA CGCGACTTGA AACAGGAGCT TTTGATGGGA GGCCAGCAGA CTATTTATTC      300
      ATGCTCCTCT TTAAGTGGAT TTGCATCGTG ATTACTGGCT TAGCAATGGA TATGCAGTTG      360
      CTGATGATTC CTCTGATCAT GTCAGTACTT TATGTCTGGG CCCAGCTGAA CAGAGACATG      420
10   ATTGTATCAT TTTGGTTTGG AACACGATTT AAGGCCTGCT ATTTACCCTG GGTTATCCTT      480
      GGATTCAACT ATATCATCGG AGGCTCGGTA ATCAATGAGC TTATTGAAA TCTGGTTGGA      540
      CATCTTTATT TTTTCCTAAT GTTCAGATAC CCAATGGACT TGGGAGGAAG AAATTTTCTA      600
      TCCACACCTC AGTTTTTGTG CCGCTGGCTG CCCAGTAGGA GAGGAGGAGT ATCAGGATTT      660
      GGTGTGCCCC CTGCTAGCAT GAGGCGAGCT GCTGATCAGA ATGGCGGAGG CGGGAGACAC      720
15   AACTGGGGCC AGGGCTTTCG ACTTGAGAC CAG                                     753

```

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

```

20   (A) LENGTH: 318
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

## (ii) SEQUENCE KIND: cDNA to mRNA

25

## (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Homo sapiens
      (B) CELL KIND: Epidermoid carcinoma
      (C) CELL LINE: KB
30   (D) CLONE NAME: HP10389

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

      ATGGCGACTC CCGGCCCTGT GATTCCGGAG GTCCCTTTG AACCATCGAA GCCTCCAGTC      60
35   ATTGAGGGGC TGAGCCCCAC TGTTTACAGG AATCCAGAGA GTTCAAGGA AAAGTTCGTT      120
      CGCAAGACCC GCGAGAACCC GGTGGTACCC ATAGGTTGCC TGGCCACGGC GGCCGCCCTC      180
      ACCTACGGCC TCTACTCCTT CCACCGGGGC AACAGCCAGC GCTCTCAGCT CATGATGCGC      240
      ACCCGGATCG CCGCCCAGGG TTTCACGGTC GCAGCCATCT TGCTGGGTCT GGCTGTCACT      300

```

GCTATGAAGT CTCGACCC

318

## (2) INFORMATION FOR SEQ ID NO: 26:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 10 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10408

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

	ATGGGGTCTG GGCTGCCCCT TGTCTCCTC TTGACCCTCC TTGGCAGCTC ACATGGAACA	60
20	GGGCCGGGTA TGACTTTGCA ACTGAAGCTG AAGGAGTCTT TTCTGACAAA TTCCTCCTAT	120
	GAGTCCAGCT TCCTGGAATT GCTTGAAAAG CTCTGCCTCC TCCTCCATCT CCCTTCAGGG	180
	ACCAGCGTCA CCCTCCACCA TGCAAGATCT CAACACCATG TTGTCTGCAA CACA	234

## 25 (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 30 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10412

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

	ATGGTGGCGC CTGTGTGGTA CTTGGTAGCG GCGGCTCTGC TAGTCGGCTT TATCCTCTTC	60
	CTGACTCGCA GCCGGGGCCG GCGGGCATCA GCCGGCCAAG AGCCACTGCA CAATGAGGAG	120
	CTGGCAGGAG CAGGCCGGGT GGCCAGCCT GGGCCCTGG AGCCTGAGGA GCCGAGAGCT	180
	GGAGGCAGGC CTCGGCGCCG GAGGGACCTG GGCAGCCGCC TACAGGCCCA GCGTCGAGOC	240
5	CAGCGGTGG CCTGGGCAGA AGCAGATGAG AACGAGGAGG AAGCTGTCAT CCTAGCCCAG	300
	GAGGAGGAAG GTGTCGAGAA GCCAGCGGAA ACTCACCTGT CGGGGAAAAT TGGAGCTAAG	360
	AAACTGCGGA AGCTGGAGGA GAAACAAGCG CGAAAGGCC AGCGTGAGGC AGAGGAGGCT	420
	GAACGTGAGG AGCGGAAACG ACTCGAGTCC CAGCGCGAAG CTGAGTGGA GAAGGAGGAG	480
	GAGCGGCTTC GCCTGGAGGA GGAGCAGAAG GAGGAGGAGG AGAGGAAGGC CCGCGAGGAG	540
10	CAGGCCCAGC GGGAGCATGA GGAGTACCTG AACTGAAGG AGGCCTTTGT GGTGGAGGAG	600
	GAAGGCGTAG GAGAGACCAT GACTGAGGAA CAGTCCCAGA GCTTCCTGAC AGAGTTTCATC	660
	AACTACATCA AGCAGTCCAA GGTGTGCTC TTGAAGACC TGGCTTCCA GGTGGGCCTA	720
	CGCACTCAGG ACACCATAAA TCGCATCCAG GACCTGCTGG CTGAGGGGAC TATAACAGGT	780
	GTGATTGACG ACCGGGGCAA GTTCATCTAC ATAACCCAG AGGAACTGGC CGCCGTGGCC	840
15	AACTTCATCC GACAGCGGGG CCGGGTGTCC ATCGCCGAGC TTGCCCAAGC CAGCAACTCC	900
	CTCATCGCCT GGGGCCGGGA GTCCCCTGCC CAAGCCCCAG CC	942

## (2) INFORMATION FOR SEQ ID NO: 28:

## 20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 25 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10413

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

	ATGGCTGCCG AGGATGTGGT GGCGACTGGC GCCGACCCAA GCGATCTGGA GAGCGGCGGG	60
35	CTGCTGCATG AGATTTTCAC GTCGCCGCTC AACCTGCTGC TGCTTGGCCT CTGCATCTTC	120
	CTGCTCTACA AGATCGTGCG CGGGGACCAG CCGCGGCCA GCGGCGACAG CGACGACGAC	180
	GAGCCGCCCC CTCTGCCCCG CCTCAAGCGG CGCGACTTCA CCCCCCGGA GCTGCGGCGC	240
	TTGACGGCG TCCAGGACCC GCGCATACTC ATGGCCATCA ACGGCAAGGT GTTCGATGTG	300

```

ACCAAAGGCC GCAAATTCTA CGGGCCCGAG GGGCCGTATG GGGTCTTTGC TGGAAGAGAT 360
GCATCCAGGG GCCTTGCCAC ATTTTGCTG GATAAGGAAG CACTGAAGGA TGAGTACGAT 420
GACCTTTCTG ACCTCACTGC TGCCAGCAG GAGACTCTGA GTGACTGGA GTCTCAGTTC 480
ACTTTCAAGT ATCATCACGT GGGCAAACG CTGAAGGAGG GGGAGGAGCC CACTGTGTAC 540
5 TCAGATGAGG AAGAACCAAA AGATGAGAGT GCGCGGAAAA ATGAT 585

```

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1386  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10415

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

ATGTTGGA CTGCGATCTT CGCCGTTACC TTCTTGCTGG CGTTGGTGGG AGCCGTGCTC 60
TACCTCTATC CGGCTTCCAG ACAAGCTGCA GGAATTCCAG GGATTACTCC AACTGAAGAA 120
25 AAAGATGGTA ATCTTCCAGA TATTGTGAAT AGTGGAAGTT TGCATGAGTT CCTGGTTAAT 180
TTGCATGAGA GATATGGGCC TGTGGTCTCC TTCTGGTTTG GCAGGCGCCT CGTGGTTAGT 240
TTGGGCACTG TTGATGTACT GAAGCAGCAT ATCAATCCCA ATAAGACATT GGACCCTTTT 300
GAAACCATGC TGAAGTCATT ATTAAGGTAT CAATCTGGTG GTGGCAGTGT GAGTGAAAAAC 360
CACATGAGGA AAAAATTGTA TGAAAATGGT GTGACTGATT CTCTGAAGAG TAACTTTGCC 420
30 CTCCTCCTAA AGCTTTCAGA AGAATTATTA GATAAATGGC TCTCCTACCC AGAGACCCAG 480
CACGTGCCCC TCAGCCAGCA TATGCTTGGT TTTGCTATGA AGTCTGTAC ACAGATGGTA 540
ATGGGTAGTA CATTTGAAGA TGATCAGGAA GTCATTCGCT TCCAGAAGAA TCATGGCACA 600
GTTTGGTCTG AGATTGGAAG AGGCTTTCTA GATGGGTCAC TTGATAAAAA CATGACTCGG 660
AAAAACAAT ATGAAGATGC CCTCATGCAA CTGGAGTCTG TTTTAAGGAA CATCATAAAA 720
35 GAACGAAAAG GAAGGAACCT CAGTCAACAT ATTTTCATTG ACTCCTTAGT ACAAGGGAAC 780
CTTAATGACC AACAGATCCT AGAAGACAGT ATGATATTTT CTCTGGCCAG TTGCATAATA 840
ACTGCAAAAT TGTGTACCTG GGCAATCTGT TTTTAAACCA CCTCTGAAGA AGTTCAAAAA 900
AAATTATATG AAGAGATAAA CCAAGTTTTT GGAAATGGTC CTGTTACTCC AGAGAAAATT 960

```

GAGCAGCTCA GATATTGTCA GCATGTGCTT TGTGAACTG TTCGAACTGC CAAACTGACT 1020  
 CCAGTTTCTG CCCAGCTTCA AGATATTGAA GGAAAAATTG ACCGATTTAT TATTCCTAGA 1080  
 GAGACCCTCG TCCTTTATGC CCTTGGTGTG GACTTTCAGG ATCCTAATAC TTGGCCATCT 1140  
 CCACACAAGT TTGATCCAGA TCGGTTTGAT GATGAATTAG TAATGAAAAC TTTTCTCTCA 1200  
 5 CTTGGATTCT CAGGCACACA GGAGTGCCA GAGTTGAGGT TTGCATATAT GGTGACCACA 1260  
 GTACTTCTTA GTGTATTGGT GAAGAGACTG CACCTACTTT CTGTGGAGGG ACAGGTTATT 1320  
 GAAACAAAGT ATGAACTGGT AACATCATCA AGGGAAGAAG CTTGGATCAC TGTCTCAAAG 1380  
 AGATAT 1386

10

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

25 ATGGGGGCTG CGGTGTTTTT CGGCTGCACT TTCGTCGCGT TCGGCCCCGGC CTTGCGGCTT 60  
 TTCTTGATCA CTGTGGCTGG GGACCCGCTT CGCGTTATCA TCCTGGTCGC AGGGGCATTT 120  
 TTCTGGCTGG TCTCCCTGCT CCTGGCCTCT GTGGTCTGGT TCATCTTGGT CCATGTGACC 180  
 GACCGGTCAG ATGCCCGGCT CCAGTACGGC CTCCTGATTT TTGGTGCTGC TGTCTCTGTC 240  
 30 CTTCTACAGG AGGTGTTCCG CTTTGCTAC TACAAGCTGC TTAAGAAGGC AGATGAGGGG 300  
 TTAGCATCGC TGAGTGAGGA CGGAAGATCA CCCATCTCCA TCCGCCAGAT GGCCTATGTT 360  
 TCTGGTCTCT CCTTCGGTAT CATCAGTGGT GTCTTCTCTG TTATCAATAT TTTGGCTGAT 420  
 GCACTTGGGC CAGGTGTGGT TGGGATCCAT GGAGACTCAC CCTATTACTT CCTGACTTCA 480  
 GCCTTTCTGA CAGCAGCCAT TATCCTGCTC CATACCTTTT GGGGAGTTGT GTTCTTTGAT 540  
 35 GCCTGTGAGA GGAGACGGTA CTGGGCTTTG GGCCTGGTGG TTGGGAGTCA CCTACTGACA 600  
 TCGGGACTGA CATTCCTGAA CCCCTGGTAT GAGGCCAGCC TGCTGCCCAT CTATGCAGTC 660  
 ACTGTTTCCA TGGGGCTCTG GGCCTTCATC ACAGCTGGAG GGTCCCTCCG AAGTATTGAG 720  
 CGCAGCCTCT TGTGTAAGGA C 741



## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339
- 5 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) SEQUENCE KIND: cDNA to mRNA

## 10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10424

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGAACTTCT	ATTTACTCCT	AGCGAGCAGC	ATTCTGTGTG	CCTTGATTGT	CTTCTGAAAA	60
TATCGCCGCT	TTCAGAGAAA	CACTGGCGAA	ATGTCATCAA	ATTCAACTGC	TCTTGCACTA	120
GTGAGACCCT	CTTCTTCTGG	GTTAATTAAC	AGCAATACAG	ACAACAATCT	TGCAGTCTAC	180
20 GACCTCTCTC	GGGATATTTT	AAATAATTTC	CCACACTCAA	TAGCCAGGCA	GAAGCGAATA	240
TTGGTAAACC	TCAGTATGGT	GGAAAACAAG	CTGGTTGAAC	TGGAACATAC	TCTACTTAGC	300
AAGGGTTTCA	GAGGTGCATC	ACCTCACCGG	AAATCCACC			339

## 25 (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 30 (D) TOPOLOGY: Linear
- (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- 35 (B) CELL KIND: Epidermoid carcinoma
- (C) CELL LINE: KB
- (D) CLONE NAME: HP10428

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

ATGGGGAGGT GGGCCCTCGA TGTGGCCTTT TTGTGGAAGG CGGTGTTGAC CCTGGGGCTG      60
GTGCTTCTCT ACTACTGCTT CTCCATCGGC ATCACCTTCT ACAACAAGTG GCTGACAAAAG      120
5 AGCTTCCATT TCCCCCTCTT CATGACGATG CTGCACCTGG CCGTGATCTT CCTCTTCTCC      180
GCCCTGTCCA GGGCGCTGGT TCAGTGCTCC AGCCACAGGG CCCGTGTGGT GCTGAGCTGG      240
GCCGACTACC TCAGAAGAGT GGCTCCCACA GCTCTGGCGA CGGCGCTTGA CGTGGGCTTG      300
TCCAACGTGA GCTTCCTGTA TGTACCCGTC TCGCTGTACA CAATGACCAA ATCCTCAGCT      360
GTCCTCTTCA TCTTGATCTT CTCTCTGATC TTCAAGCTGG AGGAGCTGCG CGCGGCACTG      420
10 GTCCTGGTGG TCCTCCTCAT CGCCGGGGGT CTCTTCATGT TCACCTACAA GTCCACACAG      480
TTCAACGTGG AGGGCTTCGC CTTGGTGCTG GGGGCCTCGT TCATCGGTGG CATTGCTGG      540
ACCCTACCCC AGATGCTCCT GCAGAAGGCT GAACTCGGCC TCCAGAATCC CATCGACACC      600
ATGTTCCACC TGCAGCCACT CATGTTCTTG GGGCTCTTCC CTCTCTTTGC TGTATTTGAA      660
GGTCTCCATT TGTCCACATC TGAGAAAATC TTCCGTTTCC AGGACACAGG GCTGCTCCTG      720
15 CGGGTACTTG GGAGCCTCTT CCTTGGCGGG ATTCTCGCCT TTGGTTTGGG CTTCTCTGAG      780
TTCCTCCTGG TCTCCAGAAC CTCCAGCCTC ACTCTCTCCA TTGCCGGCAT TTTTAAGGAA      840
GTCTGCACTT TGCTGTTGGC AGTCATCTG CTGGGCGATC AGATCAGCCT CCTGAACTGG      900
CTGGGCTTCG CCCTCTGCCT CTCGGAATA TCCCTCCACG TTGCCCTCAA AGCCCTGCAT      960
TCCAGAGGTG ATGGTGGCCC CAAGGCCTTG AAGGGGCTGG GCTCCAGCCC CGACCTGGAG      1020
20 CTGCTGCTCC GGAGCAGCCA GCGGGAGGAA GGTGACAATG AGGAGGAGGA GTACTTTGTG      1080
GCCCAGGGGC AGCAG      1095

```

## (2) INFORMATION FOR SEQ ID NO: 33:

## 25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## 30 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

## 35 (D) CLONE NAME: HP10429

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATGCCTACCA CAAAGAAGAC ATTGATGTTT TTATCAAGCT TTTTCACCAG CCTTGGGTCC 60  
 TTCATTGTAA TTTGCTCTAT TCTTGGGACA CAAGCATGGA TCACCAGTAC AATTGCTGTT 120  
 AGAGACTCTG CTTCAAATGG GAGCATT TTC TTTTCG TGGGGAGAGT 180  
 AGTGAAGAAT TGAGTCACGG ACTTGCAGAA CCAAAGAAAA AGTTTGCAGT TTTAGAGATA 240  
 5 CTGAATAATT CTTCCCAAAA AACTCTGCAT TCGGTGACTA TCCTGTTTCT GGTCTGAGT 300  
 TTGATCACGT CGCTGCTGAG CTCTGGGTTT ACCTTCTACA ACAGCATCAG CAACCCCTTAC 360  
 CAGACATTCC TGGGGCCGAC GGGGGTGTAC ACCTGGAACG GGCTCGGTGC ATCCTTCGTT 420  
 TTTGTGACCA TGATACTGTT TGTGGCGAAC ACGCAGTCCA ACCAACTCTC CGAAGAGTTG 480  
 TTCCAAATGC TTTACCCGGC AACCACCAGT AAAGGAACGA CCCACAGTTA CGGATACTCG 540  
 10 TTCTGGCTCA TACTGCTCGT CATTCTTCTA AATATAGTCA CTGTAACCAT CATCATTTTC 600  
 TACCAGAAGG CCAGATACCA GCGGAAGCAG GAGCAGAGAA AGCCAATGGA ATATGCTCCA 660  
 AGGGACGGAA TTTTATTC 678

15 (2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

30 ATGGCTCGGG GCTCGCTGCG CCGGTTGCTG CGGCTCCTCG TGCTGGGGCT CTGGCTGGCG 60  
 TTGCTGCGCT CCGTGGCCGG GGAGCAAGCG CCAGGCACCG CCCCCTGCTC CCGCGGCAGC 120  
 TCCTGGAGCG CGGACCTGGA CAAGTGCATG GACTGCGCGT CTTGCAGGGC GCGACCGCAC 180  
 AGCGACTTCT GCCTGGGCTG CGCTGCAGCA CCTCCTGCCC CTTCCGGCT GCTTTGGCCC 240  
 35 ATCCTTGGGG GCGCTCTGAG CCTGACCTTC GTGCTGGGGC TGCTTTCTGG CTTTTGGTC 300  
 TGGAGACGAT GCCGCAGGAG AGAGAAGTTC ACCACCCCA TAGAGGAGAC CGGCGGAGAG 360  
 GGCTGCCAG CTGTGGCGCT GATCCAG 387

## (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489  
 (B) TYPE: Nucleic acid  
 5 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Liver  
 (D) CLONE NAME: HP10433

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

15  
 ATGCGACGGC TGCTGATCCC TCTGGCCCTG TGGCTGGGCG CGGTGGGCGT GGGCGTCGCC 60  
 GAGCTCACGG AAGCCCAGCG CCGGGGCCTG CAGGTGGCCC TGGAGGAATT TCACAAGCAC 120  
 CCGCCCGTGC AGTGGGCCTT CCAGGAGACC AGTGTGGAGA GCGCCGTGGA CACGCCCTTC 180  
 CCAGCTGGAA TATTTGTGAG GCTGGAATTT AAGCTGCAGC AGACAAGCTG CCGGAAGAGG 240  
 20 GACTGGAAGA AACCCGAGTG CAAAGTCAGG CCCAATGGGA GGAAACGGAA ATGCCTGGCC 300  
 TGCATCAAAC TGGGCTCTGA GGACAAAGTT CTGGGCCGGT TGGTCCACTG CCCCATAGAG 360  
 ACCCAAGTTC TCGGGGAGGC TGAGGAGCAC CAGGAGACCC AGTGCCTCAG GGTGCAGCGG 420  
 GCTGGTGAGG ACCCCCACAG CTTCTACTTC CCTGGACAGT TCGCCTTCTC CAAGGCCCTG 480  
 CCCC GCAGC 489  
 25

## (2) INFORMATION FOR SEQ ID NO: 36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579  
 30 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10480

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

      ATGATCCGCT GCGGCCTGGC CTGCGAGCGC TGCCGCTGGA TCCTGCCCTT GCTCCTACTC      60
      AGCGCCATCG CCTTCGACAT CATCGCGCTG GCCGGCCGCG GCTGGTTGCA GTCTAGCGAC      120
5    CACGGCCAGA CGTCCTCGCT GTGGTGGAAA TGCTCCCAAG AGGGCGGCGG CAGCGGGTCC      180
      TACGAGGAGG GCTGTCAGAG CCTCATGGAG TACGCGTGGG GTAGAGCAGC GGCTGCCATG      240
      CTCTTCTGTG GCTTCATCAT CCTGGTGATC TGTTCATCC TCTCCTTCTT CGCCCTCTGT      300
      GGACCCCAAG TGCTTGCTTT CCTGAGAGTG ATTGGAGGTC TCCTTGCCCTT GGCTGCTGTG      360
      TTCCAGATCA TCTCCCTGGT AATTTACCCC GTGAAGTACA CCCAGACCTT CACCCTTCAT      420
10   GCCAACCGTG CTGTCACTTA CATCTATAAC TGGGCCTACG GCTTTGGGTG GGCAGCCACG      480
      ATTATCTGA TCGGCTGTGC CTTCTCTTTC TGCTGCCTCC CCAACTACGA AGATGACCTT      540
      CTGGGCAATG CCAAGCCCAG GTACTTCTAC ACATCTGCC      579

```

## 15 (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Liver
- (D) CLONE NAME: HP01263

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 37.. 1185
- (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

35   ACAAACCTGAC CCATCCTGGG CCTTGTTCTC CACAGA ATG GGT CTG CTC CTT CCC      54
                                   Met Gly Leu Leu Leu Pro
                                   1           5
      CTG GCA CTC TGC ATC CTA GTC CTG TGC TGC GGA GCA ATG TCT CCA CCC      102

```

	Leu	Ala	Leu	Cys	Ile	Leu	Val	Leu	Cys	Cys	Gly	Ala	Met	Ser	Pro	Pro	
				10					15					20			
	CAG	CTG	GCC	CTC	AAC	CCC	TCG	GCT	CTG	CTC	TCC	CGG	GGC	TGC	AAT	GAC	150
	Gln	Leu	Ala	Leu	Asn	Pro	Ser	Ala	Leu	Leu	Ser	Arg	Gly	Cys	Asn	Asp	
5			25					30					35				
	TCC	GAT	GTG	CTG	GCA	GTT	GCA	GGC	TTT	GCC	CTG	CGG	GAT	ATT	AAC	AAA	198
	Ser	Asp	Val	Leu	Ala	Val	Ala	Gly	Phe	Ala	Leu	Arg	Asp	Ile	Asn	Lys	
			40					45					50				
	GAC	AGA	AAG	GAT	GGC	TAT	GTG	CTG	AGA	CTC	AAC	CGA	GTG	AAC	GAC	GCC	246
10	Asp	Arg	Lys	Asp	Gly	Tyr	Val	Leu	Arg	Leu	Asn	Arg	Val	Asn	Asp	Ala	
	55				60				65						70		
	CAG	GAA	TAC	AGA	CGG	GGT	GGC	CTG	GGA	TCT	CTG	TTC	TAT	CTT	ACA	CTG	294
	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser	Leu	Phe	Tyr	Leu	Thr	Leu	
					75				80						85		
15	GAT	GTG	CTA	GAG	ACT	GAC	TGC	CAT	GTG	CTC	AGA	AAG	AAG	GCA	TGG	CAA	342
	Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu	Arg	Lys	Lys	Ala	Trp	Gln	
					90				95					100			
	GAC	TGT	GGA	ATG	AGG	ATA	TTT	TTT	GAA	TCA	GTT	TAT	GGT	CAA	TGC	AAA	390
	Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser	Val	Tyr	Gly	Gln	Cys	Lys	
20			105					110					115				
	GCA	ATA	TTT	TAT	ATG	AAC	AAC	CCA	AGT	AGA	GTT	CTC	TAT	TTA	GCT	GCT	438
	Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg	Val	Leu	Tyr	Leu	Ala	Ala	
					120			125					130				
	TAT	AAC	TGT	ACT	CTT	CGC	CCA	GTT	TCA	AAA	AAA	AAG	ATT	TAC	ATG	ACG	486
25	Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys	Lys	Lys	Ile	Tyr	Met	Thr	
	135					140				145					150		
	TGC	CCT	GAC	TGC	CCA	AGC	TCC	ATA	CCC	ACT	GAC	TCT	TCC	AAT	CAC	CAA	534
	Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr	Asp	Ser	Ser	Asn	His	Gln	
					155				160					165			
30	GTG	CTG	GAG	GCT	GCC	ACC	GAG	TCT	CTT	GCG	AAA	TAC	AAC	AAT	GAG	AAC	582
	Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala	Lys	Tyr	Asn	Asn	Glu	Asn	
					170				175					180			
	ACA	TCC	AAG	CAG	TAT	TCT	CTC	TTC	AAA	GTC	ACC	AGG	GCT	TCT	AGC	CAG	630
	Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val	Thr	Arg	Ala	Ser	Ser	Gln	
35			185					190					195				
	TGG	GTG	GTC	GGC	CCT	TCT	TAC	TTT	GTG	GAA	TAC	TTA	ATT	AAA	GAA	TCA	678
	Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu	Tyr	Leu	Ile	Lys	Glu	Ser	
					200			205					210				

	CCA TGT ACT AAA TCC CAG GCC AGC AGC TGT TCA CTT CAG TCC TCC GAC	726
	Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys Ser Leu Gln Ser Ser Asp	
	215 220 225 230	
	TCT GTG CCT GTT GGT CTT TGC AAA GGT TCT CTG ACT CGA ACA CAC TGG	774
5	Ser Val Pro Val Gly Leu Cys Lys Gly Ser Leu Thr Arg Thr His Trp	
	235 240 245	
	GAA AAG TTT GTC TCT GTG ACT TGT GAC TTC TTT GAA TCA CAG GCT CCA	822
	Glu Lys Phe Val Ser Val Thr Cys Asp Phe Phe Glu Ser Gln Ala Pro	
	250 255 260	
10	GCC ACT GGA AGT GAA AAC TCT GCT GTT AAC CAG AAA CCT ACA AAC CTT	870
	Ala Thr Gly Ser Glu Asn Ser Ala Val Asn Gln Lys Pro Thr Asn Leu	
	265 270 275	
	CCC AAG GTG GAA GAA TCC CAG CAG AAA AAC ACC CCC CCA ACA GAC TCC	918
	Pro Lys Val Glu Glu Ser Gln Gln Lys Asn Thr Pro Pro Thr Asp Ser	
15	280 285 290	
	CCC TCC AAA GCT GGG CCA AGA GGA TCT GTC CAA TAT CTT CCT GAC TTG	966
	Pro Ser Lys Ala Gly Pro Arg Gly Ser Val Gln Tyr Leu Pro Asp Leu	
	295 300 305 310	
	GAT GAT AAA AAT TCC CAG GAA AAG GGC CCT CAG GAG GCC TTT CCT GTG	1014
20	Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro Gln Glu Ala Phe Pro Val	
	315 320 325	
	CAT CTG GAC CTA ACC ACG AAT CCC CAG GGA GAA ACC CTG GAT ATT TCC	1062
	His Leu Asp Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser	
	330 335 340	
25	TTC CTC TTC CTG GAG CCT ATG GAG GAG AAG CTG GTT GTC CTG CCT TTC	1110
	Phe Leu Phe Leu Glu Pro Met Glu Glu Lys Leu Val Val Leu Pro Phe	
	345 350 355	
	CCC AAA GAA AAA GCA CGC ACT GCT GAG TGC CCA GGG CCA GCC CAG AAT	1158
	Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn	
30	360 365 370	
	GCC AGC CCT CTT GTC CTT CCG CCA TGAGAATCAC ACAGAGTCTT CTGTAGGG	1210
	Ala Ser Pro Leu Val Leu Pro Pro	
	375 380	
	GTATGGTGCG CCGCATGACA TGGGAGGCCA TGGGGACGAT GGACAGAGAC AGAGCGTGCA	1270
35	CACGTAGAGT GGCTAGTGAA GGACGCCTTT TTGACTCTTC TTGGTCTCAG CATGTTGACT	1330
	GGGATTGGAA ATAATGAGAC TGAGCCCTCG GCTTGGGCTG CACTCTACCC TGTACACTGC	1390
	CTTGTACCCT GAGCTGCATC ACCTCCTAAA CTGAGCAGTC TCATACCATG GAGAGATGCC	1450
	TCTCTTATGT CTTCAGCCAC TCACTTATAA AGATACTTAT CTTTTCAGCA GT	1502

## (2) INFORMATION FOR SEQ ID NO: 38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349
- 5 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) SEQUENCE KIND: cDNA to mRNA

## 10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Liver
- (D) CLONE NAME: HP01299

15

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 111.. 1064
- (C) CHARACTERIZATION METHOD: E

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AGCAGTTGGG GCAGGAGGAA GCCGACTGCT GCCTGGTCTG CAAAGAAGTC CTTTCAAGTC 60

TCTAGGACTG GACTCTTCCT AAGCAAGTCC GAGAAGGAAG CACCCTCACT ATG TGG 116

25 Met Trp

1

CTC TAC CTG GCG GCC TTC GTG GGC CTG TAC TAC CTT CTG CAC TGG TAC

164

Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His Trp Tyr

30 5 10 15

CGG GAG AGG CAG GTG GTG AGC CAC CTC CAA GAC AAG TAT GTC TTT ATC 212

Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val Phe Ile

20 25 30

ACG GGC TGT GAC TCG GGC TTT GGG AAC CTG CTG GCC AGA CAG CTG GAT 260

35 Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln Leu Asp

35 40 45 50

GCA CGA GGC TTG AGA GTG CTG GCT GCG TGT CTG ACG GAG AAG GGG GCC 308

Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys Gly Ala



		55		60		65		
		GAG CAG CTG AGG GGC CAG ACG TCT GAC AGG CTG GAG ACG GTG ACC CTG						356
		Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val Thr Leu						
		70		75		80		
5		GAT GTT ACC AAG ATG GAG AGC ATC GCT GCA GCT ACT CAG TGG GTG AAG						404
		Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp Val Lys						
		85		90		95		
		GAG CAT GTG GGG GAC AGA GGA CTC TGG GGA CTG GTG AAC AAT GCA GGC						452
		Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn Ala Gly						
10		100		105		110		
		ATT CTT ACA CCA ATT ACC TTA TGT GAG TGG CTG AAC ACT GAG GAC TCT						500
		Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu Asp Ser						
		115		120		125		130
		ATG AAT ATG CTC AAA GTG AAC CTC ATT GGT GTG ATC CAG GTG ACC TTG						548
15		Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val Thr Leu						
		135		140		145		
		AGC ATG CTT CCT TTG GTG AGG AGA GCA CGG GGA AGA ATT GTC AAT GTC						596
		Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val Asn Val						
		150		155		160		
20		TCC AGC ATT CTG GGA AGA GTT GCT TTC TTT GTA GGA GGC TAC TGT GTC						644
		Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr Cys Val						
		165		170		175		
		TCC AAG TAT GGA GTG GAA GCC TTT TCA GAT ATT CTG AGG CGT GAG ATT						692
		Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg Glu Ile						
25		180		185		190		
		CAA CAT TTT GGG GTG AAA ATC AGC ATA GTT GAA CCT GGC TAC TTC AGA						740
		Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr Phe Arg						
		195		200		205		210
		ACG GGA ATG ACA AAC ATG ACA CAG TCC TTA GAG CGA ATG AAG CAA AGT						788
30		Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys Gln Ser						
		215		220		225		
		TGG AAA GAA GCC CCC AAG CAT ATT AAG GAG ACC TAT GGA CAG CAG TAT						836
		Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln Gln Tyr						
		230		235		240		
35		TTT GAT GCC CTT TAC AAT ATC ATG AAG GAA GGG CTG TTG AAT TGT AGC						884
		Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu L u Asn Cys Ser						
		245		250		255		
		ACA AAC CTG AAC CTG GTC ACT GAC TGC ATG GAA CAT GCT CTG ACA TCG						932

	Thr	Asn	Leu	Asn	Leu	Val	Thr	Asp	Cys	Met	Glu	His	Ala	Leu	Thr	Ser	
	260						265						270				
	GTG	CAT	CCG	CGA	ACT	CGA	TAT	TCA	GCT	GGC	TGG	GAT	GCT	AAA	TTT	TTC	980
	Val	His	Pro	Arg	Thr	Arg	Tyr	Ser	Ala	Gly	Trp	Asp	Ala	Lys	Phe	Phe	
5	275					280					285				290		
	TTC	ATC	CCT	CTA	TCT	TAT	TTA	CCT	ACA	TCA	CTG	GCA	GAC	TAC	ATT	TTG	1028
	Phe	Ile	Pro	Leu	Ser	Tyr	Leu	Pro	Thr	Ser	Leu	Ala	Asp	Tyr	Ile	Leu	
					295					300				305			
	ACT	AGA	TCT	TGG	CCC	AAA	CCA	GCC	CAG	GCA	GTC	TAAAGAAAAC	TGGGTTGGT				1080
10	Thr	Arg	Ser	Trp	Pro	Lys	Pro	Ala	Gln	Ala	Val						
					310					315							
	GCTTCTTGGA	ATGAAGGCAA	AAATCTGAAA	TTGTTAGTGT	CTCAGTAATC	CTGATTTAGA											1140
	ACCCAGGCTT	TTTGTAACAA	TGTGTTTTCT	TGCCTAAATT	CATTTATCTG	GCATCATCAG											1200
	AGTACTAACA	TGTTTATATT	TCAGATATCC	AAAGCTTACC	ACTTTAGGTG	ATGAATCTTT											1260
15	ACTATTTTAG	CCCTTTTTTG	ATGAGACTAT	TTGTCTAAAG	TGAATCATTT	GTTCTTGCCT											1320
	TATTAAACAG	AGTAGATGGA	AAACAATTT														1349

## (2) INFORMATION FOR SEQ ID NO: 39:

## 20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1643

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## 25 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

## 30 (D) CLONE NAME: HP01347

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 25.. 915

## 35 (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

	AACATCTGGG GACAGCGGGA AAAC ATG AGT GAC TCC AAG GAA CCA AGG GTG	51
	Met Ser Asp Ser Lys Glu Pro Arg Val	
	1 5	
	CAG CAG CTG GGC CTC CTG GGG TGT CTT GGC CAT GGC GCC CTG GTG CTG	99
5	Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu	
	10 15 20 25	
	CAA CTC CTC TCC TTC ATG CTC TTG GCT GGG GTC CTG GTG GCC ATC CTT	147
	Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu	
	30 35 40	
10	GTC CAA GTG TCC AAG GTC CCC AGC TCC CTA AGT CAG GAA CAA TCC GAG	195
	Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu	
	45 50 55	
	CAA GAC GCA ATC TAC CAG AAC CTG ACC CAG CTT AAA GCT GCA GTG GGT	243
	Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly	
15	60 65 70	
	GAG CTC TCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACC	291
	Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr	
	75 80 85	
	CAG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG	339
20	Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln	
	90 95 100 105	
	GAG ATC TAC CAG GAG CTG ACC CGG CTG AAG GCT GCA GTG GGT GAG TTG	387
	Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu	
	110 115 120	
25	CCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACC CGG CTG	435
	Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu	
	125 130 135	
	AAG GCT GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG GAG ATC	483
	Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile	
30	140 145 150	
	TAC CAG GAG CTG ACC CGG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAG	531
	Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	
	155 160 165	
	AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACG GAG CTG AAG GCT	579
35	Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala	
	170 175 180 185	
	GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG	627
	Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln	

		190		195		200	
		GAG CTG ACC CAG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAC CAG TCC					675
		Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser					
		205		210		215	
5		AAG CAG CAG CAA ATC TAT CAA GAA CTG ACC GAT TTG AAG ACT GCA TTT					723
		Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe					
		220		225		230	
		GAA CGC CTG TGC CGC CAC TGT CCC AAG GAC TGG ACA TTC TTC CAA GGA					771
		Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly					
10		235		240		245	
		AAC TGT TAC TTC ATG TCT AAC TCC CAG CGG AAC TGG CAC GAC TCC GTC					819
		Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val					
		250		255		260	
		ACC GCC TGC CAG GAA GTG AGG GCC CAG CTC GTC GTA ATC AAA ACT GCT					867
15		Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala					
		270		275		280	
		GAG GAG CAG CTT CCA GCG GTA CTG GAA CAG TGG AGA ACC CAA CAA					912
		Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln					
		285		290		295	
20		TAGCGGGAAT GAAGACTGTG CGGAATTTAG TGGCAGTGGC TGGAAACGACA ATCGATGT					970
		GACGTTGACA ATTACTGGAT CTGCAAAAAG CCCGCAGCCT GCTTCAGAGA CGAATAGTTG					1030
		TTTCCCTGCT AGCCTCAGCC TCCATTGTGG TATAGCAGAA CTTCACCCAC TTGTAAGCCA					1090
		GCGCTTCTTC TCTCCATCCT TGGACCTTCA CAAATGCCCT GAGACGGTTC TCTGTTCGAT					1150
		TTTTCATCCC CTATGAACCT GGGTCTTATT CTGTCCTTCT GATGCCTCCA AGTTTCCCTG					1210
25		GTGTAGAGCT TGTGTTCTTG GCCCATCCTT GGAGCTTTAT AAGTGACCTG AGTGGGATGC					1270
		ATTTAGGGGG CGGGCTTGGT ATGTTGTATG AATCCACTCT CTGTTCTTTT TGGAGATTAG					1330
		ACTATTTGGA TTCATGTGTA GCTGCCCTGT CCCCTGGGGC TTTATCTCAT CCATGCAAAC					1390
		TACCATCTGC TCAACTTCCA GCTACACCCC GTGCACCCTT TTGACTGGGG ACTTGCTGGT					1450
		TGAAGGAGCT CATCTTGAG GCTGGAAGCA CCAGGGAATT AATTCCCCCA GTCAACCAAT					1510
30		GGCATCCAGA GAGGGCATGG AGGCTCCATA CAACCTCTTC CACCCCCACA TCTTTCTTTG					1570
		TCCTATACAT GTCTTCCATT TGGCTGTTTC TGAGTTGTAG CCTTTATAAT AAAGTGGTAA					1630
		ATGTTGTAAC TGC					1643

35 (2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729

(B) TYPE: Nucleic acid

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01440

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10      (ix) SEQUENCE CHARACTERISTICS:
          (A) CHARACTERIZATION CODE: CDS
          (B) EXISTENCE POSITION: 38.. 631
          (C) CHARACTERIZATION METHOD: E

```

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

	ACTTTC	ACTC	ACCGC	CTGTC	CTTCCT	GACA	CCTCACC	ATG	TGT	ACG	GGA	AAA	TGT	55			
								Met	Cys	Thr	Gly	Lys	Cys				
								1					5				
20	GCC	CGC	TGT	GTG	GGG	CTC	TCC	CTC	ATT	ACC	CTC	TGC	CTC	GTC	TGC	ATT	103
	Ala	Arg	Cys	Val	Gly	Leu	Ser	Leu	Ile	Thr	Leu	Cys	Leu	Val	Cys	Ile	
				10				15						20			
	GTG	GCC	AAC	GCC	CTC	CTG	CTG	GTA	CCT	AAT	GGG	GAG	ACC	TCC	TGG	ACC	151
	Val	Ala	Asn	Ala	Leu	Leu	Leu	Val	Pro	Asn	Gly	Glu	Thr	Ser	Trp	Thr	
25				25				30						35			
	AAC	ACC	AAC	CAT	CTC	AGC	TTG	CAA	GTC	TGG	CTC	ATG	GGC	GGC	TTC	ATT	199
	Asn	Thr	Asn	His	Leu	Ser	Leu	Gln	Val	Trp	Leu	Met	Gly	Gly	Phe	Ile	
				40				45						50			
	GGC	GGG	GGC	CTA	ATG	GTA	CTG	TGT	CCG	GGG	ATT	GCA	GCC	GTT	CGG	GCA	247
30	Gly	Gly	Gly	Leu	Met	Val	Leu	Cys	Pro	Gly	Ile	Ala	Ala	Val	Arg	Ala	
				55				60						65		70	
	GGG	GGC	AAG	GGC	TGC	TGT	GGT	GCT	GGG	TGC	TGT	GGA	AAC	CGC	TGC	AGG	295
	Gly	Gly	Lys	Gly	Cys	Cys	Gly	Ala	Gly	Cys	Cys	Gly	Asn	Arg	Cys	Arg	
					75					80					85		
35	ATG	CTG	CGC	TCG	GTC	TTC	TCC	TCG	GCG	TTC	GGG	GTG	CTT	GGT	GCC	ATC	343
	Met	Leu	Arg	Ser	Val	Phe	Ser	Ser	Ala	Phe	Gly	Val	Leu	Gly	Ala	Ile	
					90					95					100		
	TAC	TGC	CTC	TCG	GTG	TCT	GGA	GCT	GGG	CTC	CGA	AAT	GGA	CCC	AGA	TGC	391

Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu Arg Asn Gly Pro Arg Cys  
 105 110 115  
 TTA ATG AAC GGC GAG TGG GGC TAC CAC TTC GAA GAC ACC GCG GGA GCT 439  
 Leu Met Asn Gly Glu Trp Gly Tyr His Phe Glu Asp Thr Ala Gly Ala'  
 5 120 125 130  
 TAC TTG CTC AAC CGC ACT CTA TGG GAT CGG TGC GAG GCG CCC CCT CGC 487  
 Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg Cys Glu Ala Pro Pro Arg  
 135 140 145 150  
 GTG GTC CCC TGG AAT GTG ACG CTC TTC TCG CTG CTG GTG GCC GCC TCC 535  
 10 Val Val Pro Trp Asn Val Thr Leu Phe Ser Leu Leu Val Ala Ala Ser  
 155 160 165  
 TGC CTG GAG ATA GTA CTG TGT GGG ATC CAG CTG GTG AAC GCG ACC ATT 583  
 Cys Leu Glu Ile Val Leu Cys Gly Ile Gln Leu Val Asn Ala Thr Ile  
 170 175 180  
 15 GGT GTC TTC TGC GGC GAT TGC AGG AAA AAA CAG GAC ACC CCT CAC TG 630  
 Gly Val Phe Cys Gly Asp Cys Arg Lys Lys Gln Asp Thr Pro His  
 185 190 195  
 AGGCTCCACT GACCGCCGGG TTACACCTGC TCCTTCCTGG ACGCCTACCT GGCTCGCTCA 690  
 CTCCTTGCT CGCTAGAATA AACTGCTTTG CGCTCTCTT 729  
 20

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322  
 25 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP01526

## 35 (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 84.. 749  
 (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

	GAGCCGCAGG TCTGGGCTGC AGTAGGTCCC GGCAACCGCA GGCTCGCGGC GGGCGCTGGG	60
	CGCGGGATCC GACTCTAGTC GTA ATG GAG GCG GGC GGC TTT CTG GAC TCG CTC	113
5	Met Glu Ala Gly Gly Phe Leu Asp Ser Leu	
	1 5 10	
	ATT TAC GGA GCA TGC GTG GTC TTC ACC CTT GGC ATG TTC TCC GCC GGC	161
	Ile Tyr Gly Ala Cys Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly	
	15 20 25	
10	CTC TCG GAC CTC AGG CAC ATG CGA ATG ACC CGG AGT GTG GAC AAC GTC	209
	Leu Ser Asp Leu Arg His Met Arg Met Thr Arg Ser Val Asp Asn Val	
	30 35 40	
	CAG TTC CTG CCC TTT CTC ACC ACG GAA GTC AAC AAC CTG GGC TGG CTG	257
	Gln Phe Leu Pro Phe Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu	
15	45 50 55	
	AGT TAT GGG GCT TTG AAG GGA GAC GGG ATC CTC ATC GTC GTC AAC ACA	305
	Ser Tyr Gly Ala Leu Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr	
	60 65 70	
	GTG GGT GCT GCG CTT CAG ACC CTG TAT ATC TTG GCA TAT CTG CAT TAC	353
20	Val Gly Ala Ala Leu Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr	
	75 80 85 90	
	TGC CCT CGG AAG CGT GTT GTG CTC CTA CAG ACT GCA ACC CTG CTA GGG	401
	Cys Pro Arg Lys Arg Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly	
	95 100 105	
25	GTC CTT CTC CTG GGT TAT GGC TAC TTT TGG CTC CTG GTA CCC AAC CCT	449
	Val Leu Leu Leu Gly Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro	
	110 115 120	
	GAG GCC CGG CTT CAG CAG TTG GGC CTC TTC TGC AGT GTC TTC ACC ATC	497
	Glu Ala Arg Leu Gln Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile	
30	125 130 135	
	AGC ATG TAC CTC TCA CCA CTG GCT GAC TTG GCT AAG GTG ATT CAA ACT	545
	Ser Met Tyr Leu Ser Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr	
	140 145 150	
	AAA TCA ACC CAA TGT CTC TCC TAC CCA CTC ACC ATT GCT ACC CTT CTC	593
35	Lys Ser Thr Gln Cys Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu	
	155 160 165 170	
	ACC TCT GCC TCC TGG TGC CTC TAT GGG TTT CGA CTC AGA GAT CCC TAT	641
	Thr Ser Ala Ser Trp Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr	

130

		175		180		185		
	ATC	ATG	GTG	TCC	AAC	TTT	CCA GGA ATC GTC ACC AGC TTT ATC CGC TTC	689
	Ile	Met	Val	Ser	Asn	Phe	Pro Gly Ile Val Thr Ser Phe Ile Arg Phe	
			190			195		200
5	TGG	CTT	TTC	TGG	AAG	TAC	CCC CAG GAG CAA GAC AGG AAC TAC TGG CTC	737
	Trp	Leu	Phe	Trp	Lys	Tyr	Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu	
		205		210		215		
	CTG	CAA	ACC	TGAGGCTGCT	CATCTGACCA	CTGGGCACCT	TAGTGCCAAC CTGA	790
	Leu	Gln	Thr					
10		220						
	ACCAAAGAGA	CCTCCTTGTT	TCAGCTGGGC	CTGCTGTCCA	GCTTCCCAGG	TGCAGTGGGT		850
	TGTGGGAACA	AGAGATGACT	TTGAGGATAA	AAGGACCAAA	GAAAAAGCTT	TACTTAGATG		910
	ATTGATTGGG	GCCTAGGAGA	TGAAATCACT	TTTTATTTTT	TAGAGATTTT	TTTTTTTAAT		970
	TTTGGAGGTT	GGGGTGCAAT	CTTTAGAATA	TGCCTTAAAA	GGCCGGGCGC	GGTGGCTCAC		1030
15	GCCTGTAATC	CCAGCACTTT	GGGAGGCCAA	GGTGGGCGGA	TCGCCTGAGG	TCAGGAGTTC		1090
	AAGACCAACC	TGACTAACAT	GGTGAAACCC	CATCTCTACT	AAAAATACAA	AATTAGCCAG		1150
	GCATGATGGC	ACATGCCTGT	AATCCCAGAT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT		1210
	GAACCCAGGA	GGTGGAGGTT	GCAGTGAGCT	GAGATCGTGC	CATTGTGATA	TGAATATGCC		1270
	TTATATGCTG	ATATGAATAT	GCCTTAAAAAT	AAAGTGTTCC	CCACCCTGCT	CC		1322
20								

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3045
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10230

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 191.. 946
- (C) CHARACTERIZATION METHOD: E



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

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GTTTCGCCTC AGAAGGCTGC CTCGCTGGTC CGAATTCGGT GCGGCCACGT CCGCCCGTCT      60
CCGCCTTCTG CATCGCGGCT TCGGCGGCTT CCACCTAGAC ACCTAACAGT CGCGGAGCCG      120
5  GCGCGTCGT GAGGGGGTCG GCACGGGGAG TCGGGCGGTC TTGTGCATCT TGGCTACCTG      180
TGGGTCGAAG ATG TCG GAC ATC GGA GAC TGG TTC AGG AGC ATC CCG GCG      229
      Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala
              1              5              10
ATC ACG CGC TAT TGG TTC GCC GCC ACC GTC GCC GTG CCC TTG GTC GGC      277
10  Ile Thr Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly
      15              20              25
AAA CTC GGC CTC ATC AGC CCG GCC TAC CTC TTC CTC TGG CCC GAA GCC      325
Lys Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala
      30              35              40              45
15  TTC CTT TAT CGC TTT CAG ATT TGG AGG CCA ATC ACT GCC ACC TTT TAT      373
Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr
              50              55              60
TTC CCT GTG GGT CCA GGA ACT GGA TTT CTT TAT TTG GTC AAT TTA TAT      421
Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr
20  TTC TTA TAT CAG TAT TCT ACG CGA CTT GAA ACA GGA GCT TTT GAT GGG      469
Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly
      80              85              90
AGG CCA GCA GAC TAT TTA TTC ATG CTC CTC TTT AAC TGG ATT TGC ATC      517
25  Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile
      95              100              105
GTG ATT ACT GGC TTA GCA ATG GAT ATG CAG TTG CTG ATG ATT CCT CTG      565
Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu
      110              115              120              125
30  ATC ATG TCA GTA CTT TAT GTC TGG GCC CAG CTG AAC AGA GAC ATG ATT      613
Ile Met Ser Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile
              130              135              140
GTA TCA TTT TGG TTT GGA ACA CGA TTT AAG GCC TGC TAT TTA CCC TGG      661
Val Ser Phe Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp
35  GTA TCA TTT TGG TTT GGA ACA CGA TTT AAG GCC TGC TAT TTA CCC TGG      661
Val Ser Phe Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp
              145              150              155
GTT ATC CTT GGA TTC AAC TAT ATC ATC GGA GGC TCG GTA ATC AAT GAG      709
Val Ile Leu Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu
              160              165              170

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	CTT ATT GGA AAT CTG GTT GGA CAT CTT TAT TTT TTC CTA ATG TTC AGA	757
	Leu Ile Gly Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg	
	175 180 185	
	TAC CCA ATG GAC TTG GGA GGA AGA AAT TTT CTA TCC ACA CCT CAG TTT	805
5	Tyr Pro Met Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe	
	190 195 200 205	
	TTG TAC CGC TGG CTG CCC AGT AGG AGA GGA GGA GTA TCA GGA TTT GGT	853
	Leu Tyr Arg Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly	
	210 215 220	
10	GTG CCC CCT GCT AGC ATG AGG CGA GCT GCT GAT CAG AAT GGC GGA GGC	901
	Val Pro Pro Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly	
	225 230 235	
	GGG AGA CAC AAC TGG GGC CAG GGC TTT CGA CTT GGA GAC CAG TGAAGGG	950
	Gly Arg His Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln	
15	240 245 250	
	GCGGCCTCGG GCAGCCGCTC CTCTCAAGCC ACATTTCTCTC CCAGTGCTGG GTGCGCTTAA	1010
	CAACTGCGTT CTGGCTAACA CTGTTGGACC TGACCCACAC TGAATGTAGT CTTTCAGTAC	1070
	GAGACAAAGT TTCTTAAATC CCGAAGAAAA ATATAAGTGT TCCACAAGTT TCACGATTCT	1130
	CATTCAAGTC CTTACTGCTG TGAAGAACAA ATACCAACTG TGCAAATTGC AAAACTGACT	1190
20	ACATTTTTTG GTGTCTTCTC TTCTCCCCTT TCCGTCTGAA TAATGGGTTT TAGCGGGTCC	1250
	TAGTCTGCTG GCATTGAGCT GGGGCTGGGT CACCAAACCC TTCCCAAAG GACCCTTATC	1310
	TCTTTCTTGC ACACATGCCT CTCTCCCACT TTTCCCAACC CCCACATTTG CAACTAGAAG	1370
	AGGTTGCCCA TAAAATTGCT CTGCCCTTGA CAGGTTCTGT TATTTATTGA CTTTGGCCAA	1430
	GGCTTGGTCA CAACAATCAT ATTCACGTAA TTTTCCCCTT TTGGTGGCAG AACTGTAGCA	1490
25	ATAGGGGGAG AAGACAAGCA GCGGATGAAG CGTTTTCTCA GCTTTTGGAA TTGCTTCGAC	1550
	CTGACATCCG TTGTAACCGT TTGCCACTTC TTCAGATATT TTTATAAAAA AGTACCACTG	1610
	AGTCAGTGAG GGCCACAGAT TGGTATTAAT GAGATACGAG GGTGTGTGCT GGGTGTTTGT	1670
	TTCCTGAGCT AAGTGATCAA GACTGTAGTG GAGTTGCAGC TAACATGGGT TAGGTTTAAA	1730
	CCGTGGGGGA TGCAACCCCT TTGCGTTTCA TATGTAGGCC TACTGGCTTT GTGTAGCTGG	1790
30	AGTAGTTGGG TTGCTTTGTG TTAGGAGGAT CCAGATCATG TTGGCTACAG GGAGATGCTC	1850
	TCTTTGAGAG GCTCCTGGGC ATTGATTCCA TTTCAATCTC ATTCTGGATA TGTGTTCAAT	1910
	GAGTAAAGGA GGAGAGACCC TCATACGCTA TTTAAATGTC ACTTTTTTGC CTATCCCCCG	1970
	TTTTTTGGTC ATGTTTCAAT TAATTGTGAG GAAGGCGCAG CTCCTCTCTG CACGTAGATC	2030
	ATTTTTTAAA GCTAATGTAA GCACATCTAA GGAATAACA TGATTTAAGG TTGAAATGGC	2090
35	TTTAGAATCA TTTGGGTTTG AGGGTGTGTT ATTTTGAGTC ATGAATGTAC AAGCTCTGTG	2150
	AATCAGACCA GCTTAAATAC CCACACCTTT TTTTCGTAGG TGGGCTTTTC CTATCAGAGC	2210
	TTGGCTCATA ACCAAATAAA GTTTTTTGAA GGCCATGGCT TTTCACACAG TTATTTTATT	2270
	TTATGACGTT ATCTGAAAGC AGACTGTTAG GAGCAGTATT GAGTGGCTGT CACACTTTGA	2330

GGCAACTAAA AAGGCTTCAA ACGTTTTGAT CAGTTTCTTT TCAGGAAACA TTGTGCTCTA 2390  
 ACAGTATGAC TATTCTTTCC CCCACTCTTA AACAGTGTGA TGTGTGTTAT CCTAGGAAAT 2450  
 GAGAGTTGGC AAACAACCTC TCATTTTGAA TAGAGTTTGT GTGTACCTCT CCATATTTAA 2510  
 TTTATATGAT AAAATAGGTG GGGAGAGTCT GAACCTTAAC TGTCATGTTT TGTGTTTCAT 2570  
 5 CTGTGGCCAC AATAAAGTTT ACTTGTAATA TTTTAGAGGC CATTACTCCA ATTATGTTGC 2630  
 ACGTACACTC ATTGTACAGG CGTGGAGACT CATTGTATGT ATAAGAATAT TCTGACAGTG 2690  
 AGTGACCCGG AGTCTCTGGT GTACCCTCTT ACCAGTCAGC TGCCTGCGAG CAGTCATTTT 2750  
 TTCCTAAAGG TTTACAAGTA TTTAGAACTC TTCAGTTCAG GGCAAAATGT TCATGAAGTT 2810  
 ATTCCTCTTA AACATGGTTA GGAAGCTGAT GACGTTATTG ATTTTGTCTG GATTATGTTT 2870  
 10 CTGAATAAT TTTACCAAAA CAAGCTATTT GAGTTTTGAC TTGACAAGGC AAAACATGAC 2930  
 AGTGGATTCT CTTTACAAAT TGAAAAAATA AATCCTTATT TTGTATAAAG GACTTCCCTT 2990  
 TTTGTAAACT AATCCTTTTT ATTGTAATAA ATTGTAAATT AAAATGTGCA ACTTG 3045

15 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- 25 (B) CELL KIND: Epidermoid carcinoma
- (C) CELL LINE: KB
- (D) CLONE NAME: HP10389

(ix) SEQUENCE CHARACTERISTICS:

- 30 (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 63.. 383
- (C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

35

ATGACCTTCA CCGGGAGGCT GAGGTCGAG TCCCGATTTT CTCCTGCTGC TGTGGCCCGG 60  
 AC ATG GCG ACT CCC GGC CCT GTG ATT CCG GAG GTC CCC TTT GAA CCA 107  
 Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro

	1	5	10	15	
	TCG AAG CCT CCA GTC ATT GAG GGG CTG AGC CCC ACT GTT TAC AGG AAT	155			
	Ser Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn				
	20 25 30				
5	CCA GAG AGT TTC AAG GAA AAG TTC GTT CGC AAG ACC CGC GAG AAC CCG	203			
	Pro Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro				
	35 40 45				
	GTG GTA CCC ATA GGT TGC CTG GCC ACG GCG GCC GCC CTC ACC TAC GGC	251			
	Val Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly				
10	50 55 60				
	CTC TAC TCC TTC CAC CGG GGC AAC AGC CAG CGC TCT CAG CTC ATG ATG	299			
	Leu Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met				
	65 70 75				
	CGC ACC CGG ATC GCC GCC CAG GGT TTC ACG GTC GCA GCC ATC TTG CTG	347			
15	Arg Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu				
	80 85 90 95				
	GGT CTG GCT GTC ACT GCT ATG AAG TCT CGA CCC TAAGCCCAGG GTCTGGCCTT	400			
	Gly Leu Ala Val Thr Ala Met Lys Ser Arg Pro				
	100 105				
20	GAAAGCTCCG CAGAAATGAT TCCAAAACCC AGGGAGCAAC CACTGGCCCT ACCGTGGGAC	460			
	TTACTCCCTC CTCTCCTTTG AGAGGCCCAT GTGTCGCTGG GGAGGAAGTG ACCCTTTGTG	520			
	TAACTGTAAC CGAAAGTTTT TTCAAAAATC CTAGATGCTG TTGTTTGAAT GTTACATACT	580			
	TCTATTTGTG CCACATCTCC CCTCCACTCC CCTGCTTAAT AAACCTCTAAA AATCCACTTG	640			
	TATTTAATTC AGT	653			

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## 35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10408

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 75.. 311
- (C) CHARACTERIZATION METHOD: E

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

GTAGAAACAG GCCTGTTAAG GAGAGGCCAC CGGGACTTCA GTGTCTCCTC CATCCCAGGA      60
GCGCAGTGGC CACT ATG GGG TCT GGG CTG CCC CTT GTC CTC CTC TTG ACC      110
10      Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr
           1             5             10
CTC CTT GGC AGC TCA CAT GGA ACA GGG CCG GGT ATG ACT TTG CAA CTG      158
Leu Leu Gly Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu
           15             20             25
15 AAG CTG AAG GAG TCT TTT CTG ACA AAT TCC TCC TAT GAG TCC AGC TTC      206
Lys Leu Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe
           30             35             40
CTG GAA TTG CTT GAA AAG CTC TGC CTC CTC CTC CAT CTC CCT TCA GGG      254
Leu Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
20  45             50             55             60
ACC AGC GTC ACC CTC CAC CAT GCA AGA TCT CAA CAC CAT GTT GTC TGC      302
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val Cys
           65             70             75
AAC ACA TGACAGCCAT TGAAGCCTGT GTCCTTCTTG GCCCGGGCTT TTGGGCCGGG GA      360
25 Asn Thr

TGCAGGAGGC AGGCCCGAC CCTGTCTTTC AGCAGGCCCC CACCCTCCTG AGTGGCAATA      420
AATAAAATTC GGTATGCTG      439

```

30

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10412

5

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 56.. 1000  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

	CTATGAGATC CCGGCCTCAG GGTGGACGCA GTGGTTCTGC ACTGAGGCCC TCGTC ATG	58
		Met
15		1
	GTG GCG CCT GTG TGG TAC TTG GTA GCG GCG GCT CTG CTA GTC GGC TTT	106
	Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe	
	5 10 15	
	ATC CTC TTC CTG ACT CGC AGC CGG GGC CGG GCG GCA TCA GCC GGC CAA	154
20	Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln	
	20 25 30	
	GAG CCA CTG CAC AAT GAG GAG CTG GCA GGA GCA GGC CGG GTG GCC CAG	202
	Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala Gln	
	35 40 45	
25	CCT GGG CCC CTG GAG CCT GAG GAG CCG AGA GCT GGA GGC AGG CCT CGG	250
	Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro Arg	
	50 55 60 65	
	CGC CGG AGG GAC CTG GGC AGC CGC CTA CAG GCC CAG CGT CGA GCC CAG	298
	Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala Gln	
30	70 75 80	
	CGG GTG GCC TGG GCA GAA GCA GAT GAG AAC GAG GAG GAA GCT GTC ATC	346
	Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val Ile	
	85 90 95	
	CTA GCC CAG GAG GAG GAA GGT GTC GAG AAG CCA GCG GAA ACT CAC CTG	394
35	Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His Leu	
	100 105 110	
	TCG GGG AAA ATT GGA GCT AAG AAA CTG CGG AAG CTG GAG GAG AAA CAA	442
	Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys Gln	

	115	120	125	
	GCG CGA AAG GCC CAG CGT GAG GCA GAG GAG GCT GAA CGT GAG GAG CGG			490
	Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu Arg			
	130	135	140	145
5	AAA CGA CTC GAG TCC CAG CGC GAA GCT GAG TGG AAG AAG GAG GAG GAG			538
	Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu Glu			
	150	155	160	
	CGG CTT CGC CTG GAG GAG GAG CAG AAG GAG GAG GAG GAG AGG AAG GCC			586
	Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys Ala			
10	165	170	175	
	CGC GAG GAG CAG GCC CAG CGG GAG CAT GAG GAG TAC CTG AAA CTG AAG			634
	Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu Lys			
	180	185	190	
	GAG GCC TTT GTG GTG GAG GAG GAA GGC GTA GGA GAG ACC ATG ACT GAG			682
15	Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr Glu			
	195	200	205	
	GAA CAG TCC CAG AGC TTC CTG ACA GAG TTC ATC AAC TAC ATC AAG CAG			730
	Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys Gln			
	210	215	220	225
20	TCC AAG GTT GTG CTC TTG GAA GAC CTG GCT TCC CAG GTG GGC CTA CGC			778
	Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu Arg			
	230	235	240	
	ACT CAG GAC ACC ATA AAT CGC ATC CAG GAC CTG CTG GCT GAG GGG ACT			826
	Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly Thr			
25	245	250	255	
	ATA ACA GGT GTG ATT GAC GAC CGG GGC AAG TTC ATC TAC ATA ACC CCA			874
	Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr Pro			
	260	265	270	
	GAG GAA CTG GCC GCC GTG GCC AAC TTC ATC CGA CAG CGG GGC CGG GTG			922
30	Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg Val			
	275	280	285	
	TCC ATC GCC GAG CTT GCC CAA GCC AGC AAC TCC CTC ATC GCC TGG GGC			970
	Ser Ile Ala Glu Leu Ala Gln Ala Ser Asn Ser Leu Ile Ala Trp Gly			
	290	295	300	305
35	CGG GAG TCC CCT GCC CAA GCC CCA GCC TGACCCAGT CCTTCCCTCT TGG			1020
	Arg Glu Ser Pro Ala Gln Ala Pro Ala			
	310			
	ACTCAGAGTT GGTGTGGCCT ACCTGGCTAT ACATCTTCAT CCCTCCCCAC CATCCTGGGG			1080

AAGTGATGGT GTGGCCAGGC AGTTATAGAT TAAAGGCCTG TGAGTACTGC T

1131

## (2) INFORMATION FOR SEQ ID NO: 46:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1875
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 10 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10413

15

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 79.. 666
- (C) CHARACTERIZATION METHOD: E

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	CTCGCTCGCT CAGAGGGAGG AGAAAGTGGC GAGTTCCGGA TCCCTGCCTA GCGCGGCCCA	60
25	ACCTTTACTC CAGAGATC ATG GCT GCC GAG GAT GTG GTG GCG ACT GGC GCC	111
	Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala	
	1 5 10	
	GAC CCA AGC GAT CTG GAG AGC GGC GGG CTG CTG CAT GAG ATT TTC ACG	159
	Asp Pro Ser Asp Leu Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr	
30	15 20 25	
	TCG CCG CTC AAC CTG CTG CTG CTT GGC CTC TGC ATC TTC CTG CTC TAC	207
	Ser Pro Leu Asn Leu Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr	
	30 35 40	
	AAG ATC GTG CGC GGG GAC CAG CCG GCG GCC AGC GGC GAC AGC GAC GAC	255
35	Lys Ile Val Arg Gly Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp	
	45 50 55	
	GAC GAG CCG CCC CCT CTG CCC CGC CTC AAG CGG CGC GAC TTC ACC CCC	303
	Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro	



	60	65	70	75	
	GCC GAG CTG CGG CGC TTC GAC GGC GTC CAG GAC CCG CGC ATA CTC ATG				351
	Ala Glu Leu Arg Arg Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met				
		80	85	90	
5	GCC ATC AAC GGC AAG GTG TTC GAT GTG ACC AAA GGC CGC AAA TTC TAC				399
	Ala Ile Asn Gly Lys Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr				
		95	100	105	
	GGG CCC GAG GGC CCG TAT GGG GTC TTT GCT GGA AGA GAT GCA TCC AGG				447
	Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg				
10		110	115	120	
	GGC CTT GCC ACA TTT TGC CTG GAT AAG GAA GCA CTG AAG GAT GAG TAC				495
	Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr				
		125	130	135	
	GAT GAC CTT TCT GAC CTC ACT GCT GCC CAG CAG GAG ACT CTG AGT GAC				543
15	Asp Asp Leu Ser Asp Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp				
		140	145	150	155
	TGG GAG TCT CAG TTC ACT TTC AAG TAT CAT CAC GTG GGC AAA CTG CTG				591
	Trp Glu Ser Gln Phe Thr Phe Lys Tyr His His Val Gly Lys Leu Leu				
		160	165	170	
20	AAG GAG GGG GAG GAG CCC ACT GTG TAC TCA GAT GAG GAA GAA CCA AAA				639
	Lys Glu Gly Glu Glu Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys				
		175	180	185	
	GAT GAG AGT GCC CGG AAA AAT GAT TAAAGCATTC AGTGGAAAGTA TATCTAT				690
	Asp Glu Ser Ala Arg Lys Asn Asp				
25		190	195		
	TTTTGTATTT TGCAAAATCA TTTGTAACAG TCCACTCTGT CTTTAAAACA TAGTGATTAC				750
	AATATTTTGA AAGTTTTGAG CACTTGCTAT AAGTTTTTTA TAACATCACT AGTGACACTA				810
	ATAAAATTAA CTTCTTAGAA TGCATGATGT GTTTGTGTGT CACAAATCCA GAAAGTGAAC				870
	TGCAGTGCTG TAATACACAT GTTAATACTG TTTTCTTCT ATCTGTAGTT AGTACAGGAT				930
30	GAATTTAAAT GTGTTTTTCC TGAGAGACAA GGAAGACTTG GGTATTTCCC AAAACAGGTA				990
	AAAATCTTAA ATGTGCACCA AGAGCAAAGG ATCAACTTTT AGTCATGATG TTCTGTAAAG				1050
	ACAACAAATC CCTTTTTTTT TCTCAATTGA CTTAACTGCA TGATTTCTGT TTTATCTACC				1110
	TCTAAAGCAA ATCTGCAGTG TTCCAAAGAC TTTGGTATGG ATTAAGCGCT GTCCAGTAAC				1170
	AAAATGAAAT CTCAAAACAG AGCTCAGCTG CAAAAAGCA TATTTTCTGT GTTCTGGAC				1230
35	TGCACTGTTG TCCTTGCCCT CACATAGACA CTCAGACACC CTCACAAACA CAGTAGTCTA				1290
	TAGTTAGGAT TAAAATAGGA TCTGAACATT CAAAAGAAAG CTTTGAAAAA AAAGAGCTGG				1350
	CTGGCCTAAA AACCTAAATA TATGATGAAG ATTGTAGGAC TGTCTTCCCA AGCCCCATGT				1410
	TCATGGTGGG GCAATGGTTA TTTGGTTATT TTA CTCAATT GGTTACTCTC ATTTGAAATG				1470

AGGGAGGGAC ATACAGAATA GGAACAGGTG TTTGCTCTCC TAAGAGCCTT CATGCACACC 1530  
 CCTGAACCAC GAGGAAACAG TACAGTCGCT AGTCAAGTGG TTTTAAAGT AAAGTATATT 1590  
 CATAAGGTAA CAGTTATTCT GTTGTATAA AACTATACCC ACTGCAAAAG TAGTAGTCAA 1650  
 GTGTCTAGGT CTTTGATATT GCTCTTTTGG TTAACACTAA GCTTAAGTAG ACTATACAGT 1710  
 5 TGTATGAATT TGTAAAAGTA TATGAACACC TAGTGAGATT TCAAACCTGT AATTGTGGTT 1770  
 AAATAGTCAT TGTATTTTCT TGTGAACTGT GTTTTATGAT TTTACCTCAA ATCAGAAAAC 1830  
 AAAATGATGT GCTTTGGTCA GTTAATAAAA ATGGTTTTAC CCACT 1875

10 (2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1563
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- 20 (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10415

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- 25 (B) EXISTENCE POSITION: 72.. 1460
- (C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

30 AAATTGGGCC AGGCTGAGGC GCTGCTGCTG GAGCGGCCGA TCCGAGACGT GGCTCCCTGG 60  
 GCGGCAGAAC C ATG TTG GAC TTC GCG ATC TTC GCC GTT ACC TTC TTG CTG 110  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu  
 1 5 10  
 GCG TTG GTG GGA GCC GTG CTC TAC CTC TAT CCG GCT TCC AGA CAA GCT 158  
 35 Ala Leu Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala  
 15 20 25  
 GCA GGA ATT CCA GGG ATT ACT CCA ACT GAA GAA AAA GAT GGT AAT CTT 206  
 Ala Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu

	30	35	40	45	
	CCA GAT ATT GTG AAT AGT GGA AGT TTG CAT GAG TTC CTG GTT AAT TTG				254
	Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu				
	50	55	60		
5	CAT GAG AGA TAT GGG CCT GTG GTC TCC TTC TGG TTT GGC AGG CGC CTC				302
	His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu				
	65	70	75		
	GTG GTT AGT TTG GGC ACT GTT GAT GTA CTG AAG CAG CAT ATC AAT CCC				350
	Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro				
10	80	85	90		
	AAT AAG ACA TTG GAC CCT TTT GAA ACC ATG CTG AAG TCA TTA TTA AGG				398
	Asn Lys Thr Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg				
	95	100	105		
	TAT CAA TCT GGT GGT GGC AGT GTG AGT GAA AAC CAC ATG AGG AAA AAA				446
15	Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys				
	110	115	120	125	
	TTG TAT GAA AAT GGT GTG ACT GAT TCT CTG AAG AGT AAC TTT GCC CTC				494
	Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu				
	130	135	140		
20	CTC CTA AAG CTT TCA GAA GAA TTA TTA GAT AAA TGG CTC TCC TAC CCA				542
	Leu Leu Lys Leu Ser Glu Glu Leu Leu Asp Lys Trp Leu Ser Tyr Pro				
	145	150	155		
	GAG ACC CAG CAC GTG CCC CTC AGC CAG CAT ATG CTT GGT TTT GCT ATG				590
	Glu Thr Gln His Val Pro Leu Ser Gln His Met Leu Gly Phe Ala Met				
25	160	165	170		
	AAG TCT GTT ACA CAG ATG GTA ATG GGT AGT ACA TTT GAA GAT GAT CAG				638
	Lys Ser Val Thr Gln Met Val Met Gly Ser Thr Phe Glu Asp Asp Gln				
	175	180	185		
	GAA GTC ATT CGC TTC CAG AAG AAT CAT GGC ACA GTT TGG TCT GAG ATT				686
30	Glu Val Ile Arg Phe Gln Lys Asn His Gly Thr Val Trp Ser Glu Ile				
	190	195	200	205	
	GGA AAA GGC TTT CTA GAT GGG TCA CTT GAT AAA AAC ATG ACT CGG AAA				734
	Gly Lys Gly Phe Leu Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys				
	210	215	220		
35	AAA CAA TAT GAA GAT GCC CTC ATG CAA CTG GAG TCT GTT TTA AGG AAC				782
	Lys Gln Tyr Glu Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn				
	225	230	235		
	ATC ATA AAA GAA CGA AAA GGA AGG AAC TTC AGT CAA CAT ATT TTC ATT				830

	Ile	Ile	Lys	Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	
	240						245					250					
	GAC	TCC	TTA	GTA	CAA	GGG	AAC	CTT	AAT	GAC	CAA	CAG	ATC	CTA	GAA	GAC	878
	Asp	Ser	Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	
5	255						260					265					
	AGT	ATG	ATA	TTT	TCT	CTG	GCC	AGT	TGC	ATA	ATA	ACT	GCA	AAA	TTG	TGT	926
	Ser	Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	
	270						275					280			285		
	ACC	TGG	GCA	ATC	TGT	TTT	TTA	ACC	ACC	TCT	GAA	GAA	GTT	CAA	AAA	AAA	974
10	Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys	
	290									295					300		
	TTA	TAT	GAA	GAG	ATA	AAC	CAA	GTT	TTT	GGA	AAT	GGT	CCT	GTT	ACT	CCA	1022
	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro	
	305									310					315		
15	GAG	AAA	ATT	GAG	CAG	CTC	AGA	TAT	TGT	CAG	CAT	GTG	CTT	TGT	GAA	ACT	1070
	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr	
	320									325					330		
	GTT	CGA	ACT	GCC	AAA	CTG	ACT	CCA	GTT	TCT	GCC	CAG	CTT	CAA	GAT	ATT	1118
	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	Leu	Gln	Asp	Ile	
20	335						340					345					
	GAA	GGA	AAA	ATT	GAC	CGA	TTT	ATT	ATT	CCT	AGA	GAG	ACC	CTC	GTC	CTT	1166
	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	Glu	Thr	Leu	Val	Leu	
	350						355					360			365		
	TAT	GCC	CTT	GGT	GTG	GTA	CTT	CAG	GAT	CCT	AAT	ACT	TGG	CCA	TCT	CCA	1214
25	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	Asn	Thr	Trp	Pro	Ser	Pro	
	370									375					380		
	CAC	AAG	TTT	GAT	CCA	GAT	CGG	TTT	GAT	GAT	GAA	TTA	GTA	ATG	AAA	ACT	1262
	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	Asp	Glu	Leu	Val	Met	Lys	Thr	
	385									390					395		
30	TTT	TCC	TCA	CTT	GGA	TTC	TCA	GGC	ACA	CAG	GAG	TGT	CCA	GAG	TTG	AGG	1310
	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	
	400									405					410		
	TTT	GCA	TAT	ATG	GTG	ACC	ACA	GTA	CTT	CTT	AGT	GTA	TTG	GTG	AAG	AGA	1358
	Phe	Ala	Tyr	Met	Val	Thr	Thr	Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	
35	415						420					425					
	CTG	CAC	CTA	CTT	TCT	GTG	GAG	GGA	CAG	GTT	ATT	GAA	ACA	AAG	TAT	GAA	1406
	Leu	His	Leu	Leu	Ser	Val	Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	
	430						435					440			445		

143

CTG GTA ACA TCA TCA AGG GAA GAA GCT TGG ATC ACT GTC TCA AAG AGA 1454  
 Leu Val Thr Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg  
 450 455 460  
 TAT TAAAATTTTA TACATTTAAA ATCATTGTGA AATTGATTGA GGAAAACAAC CAT 1510  
 5 Tyr  
 TTAAAAA TCTATGTTGA ATCCTTTTAT AAACCAGTAT CACTTTGTAA TAT 1563

10 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2030  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10419

20

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 171.. 914  
 (C) CHARACTERIZATION METHOD: E

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

30 CATTGGGGT TTCGGTCCC CCCCTTCCC TTCCCGGGG TCTGGGGTG ACATTGCACC 60  
 GCGCCCCTCG TGGGGTCGCG TTGCCACCCC ACGCGGACTC CCCAGCTGGC GCGCCCCTCC 120  
 CATTGCCTG TCCTGGTCAG GCCCCCACCC CCCTTCCAC CTGACCAGCC ATG GGG 176  
 Met Gly  
 1  
 35 GCT GCG GTG TTT TTC GGC TGC ACT TTC GTC GCG TTC GGC CCG GCC TTC 224  
 Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro Ala Phe  
 5 10 15  
 GCG CTT TTC TTG ATC ACT GTG GCT GGG GAC CCG CTT CGC GTT ATC ATC 272

	Ala	Leu	Phe	Leu	Ile	Thr	Val	Ala	Gly	Asp	Pro	Leu	Arg	Val	Ile	Ile	
	20						25					30					
	CTG	GTC	GCA	GGG	GCA	TTT	TTC	TGG	CTG	GTC	TCC	CTG	CTC	CTG	GCC	TCT	320
	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	Leu	Leu	Leu	Ala	Ser	
5	35						40					45				50	
	GTG	GTC	TGG	TTC	ATC	TTG	GTC	CAT	GTG	ACC	GAC	CGG	TCA	GAT	GCC	CGG	368
	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	Asp	Arg	Ser	Asp	Ala	Arg	
							55					60				65	
	CTC	CAG	TAC	GGC	CTC	CTG	ATT	TTT	GGT	GCT	GCT	GTC	TCT	GTC	CTT	CTA	416
10	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	Ala	Ala	Val	Ser	Val	Leu	Leu	
							70					75				80	
	CAG	GAG	GTG	TTC	CGC	TTT	GCC	TAC	TAC	AAG	CTG	CTT	AAG	AAG	GCA	GAT	464
	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp	
							85					90				95	
15	GAG	GGG	TTA	GCA	TCG	CTG	AGT	GAG	GAC	GGA	AGA	TCA	CCC	ATC	TCC	ATC	512
	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile	
							100					105				110	
	CGC	CAG	ATG	GCC	TAT	GTT	TCT	GGT	CTC	TCC	TTC	GGT	ATC	ATC	AGT	GGT	560
	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly	
20	115						120					125				130	
	GTC	TTC	TCT	GTT	ATC	AAT	ATT	TTG	GCT	GAT	GCA	CTT	GGG	CCA	GGT	GTG	608
	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val	
							135					140				145	
	GTT	GGG	ATC	CAT	GGA	GAC	TCA	CCC	TAT	TAC	TTC	CTG	ACT	TCA	GCC	TTT	656
25	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe	
							150					155				160	
	CTG	ACA	GCA	GCC	ATT	ATC	CTG	CTC	CAT	ACC	TTT	TGG	GGA	GTT	GTG	TTC	704
	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe	
							165					170				175	
30	TTT	GAT	GCC	TGT	GAG	AGG	AGA	CGG	TAC	TGG	GCT	TTG	GGC	CTG	GTG	GTT	752
	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val	
							180					185				190	
	GGG	AGT	CAC	CTA	CTG	ACA	TCG	GGA	CTG	ACA	TTC	CTG	AAC	CCC	TGG	TAT	800
	Gly	Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr	
35	195						200					205				210	
	GAG	GCC	AGC	CTG	CTG	CCC	ATC	TAT	GCA	GTC	ACT	GTT	TCC	ATG	GGG	CTC	848
	Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly	Leu	
							215					220				225	

TGG GCC TTC ATC ACA GCT GGA GGG TCC CTC CGA AGT ATT CAG CGC AGC 896  
 Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln Arg Ser  
 230 235 240  
 CTC TTG TGT AAG GAC TGA CTACCTG GACTGATCGC CTGACAGATC CCACCTGCC 950  
 5 Leu Leu Cys Lys Asp  
 245  
 TGTCCACTGC CCATGACTGA GCCCAGCCCC AGCCCGGGTC CATTGCCAC ATTCTCTGTC 1010  
 TCCTTCTCGT CGGTCTACCC CACTACCTCC AGGGTTTTGC TTTGTCTTTT TGTGACCGTT 1070  
 AGTCTCTAAG CTTTACCAGG AGCAGCCTGG GTTCAGCCAG TCAGTGA CTG GTGGGTTTGA 1130  
 10 ATCTGCACTT ATCCCCACCA CCTGGGGACC CCCTTGTGT GTCCAGGACT CCCCTGTGT 1190  
 CAGTGCTCTG CTCTCACCCT GCCCAAGACT CACCTCCCTT CCCCTCTGCA GGCCGACGGC 1250  
 AGGAGGACAG TCGGGTGATG GTGTATTCTG CCCTGCGCAT CCCACCCGAG GACTGAGGGA 1310  
 ACCTAGGGGG GACCCCTGGG CCTGGGGTGC CCTCCTGATG TCCTCGCCCT GTATTTCTCC 1370  
 ATCTCCAGTT CTGGACAGTG CAGGTTGCCA AGAAAAGGGA CCTAGTTTAG CCATTGCCCT 1430  
 15 GGAGATGAAA TTAATGGAGG CTCAAGGATA GATGAGCTCT GAGTTTCTCA GTACTCCCTC 1490  
 AAGACTGGAC ATCTTGGTCT TTTTCTCAGG CCTGAGGGGG AACCATTTTT GGTGTGATAA 1550  
 ATACCCTAAA CTGCCTTTTT TTCTTTTTTG AGGTGGGGGG AGGGAGGAGG TATATTGGAA 1610  
 CTCTTCTAAC CTCCTTGGGC TATATTTTCT CTCCTCGAGT TGCTCCTCAT GGCTGGGCTC 1670  
 ATTTGCGTCC CTTTCTCCTT GGTCCCAGAC CTTGGGGGAA AGGAAGGAAG TGCATGTTTT 1730  
 20 GGAAGTGGCA TTAAGTGGAA TAATGGTTTT AACCTCCTTA ACCACCAGCA TCCCTCCTCT 1790  
 CCCCAGGTG AAGTGGAGGG TGCTGTGGTG AGCTGGCCAC TCCAGAGCTG CAGTGCCACT 1850  
 GGAGGAGTCA GACTACCATG ACATCGTAGG GAAGGAGGGG AGATTTTTTT GTAGTTTTTA 1910  
 ATTGGGGTGT GGGAGGGGCG GGGAGGTTTT CTATAAACTG TATCATTTTC TGCTGAGGGT 1970  
 GGAGTGTCCC ATCCTTTTAA TCAAGGTGAT TGTGATTTTG ACTAATAAAA AAGAATTTGT 2030  
 25

## (2) INFORMATION FOR SEQ ID NO: 49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10424

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 98.. 439

(C) CHARACTERIZATION METHOD: E

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AAAGTTTCCC AAATCCAGGC GGCTAGAGGC CCACTGCTTC CCAACTACCA GCTGAGGGGG 60  
 TCCGTCCCGA GAAGGGAGAA GAGGCCGAAG AGGAAAC ATG AAC TTC TAT TTA CTC 115  
 10 Met Asn Phe Tyr Leu Leu  
 1 5  
 CTA GCG AGC AGC ATT CTG TGT GCC TTG ATT GTC TTC TGG AAA TAT CGC 163  
 Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile Val Phe Trp Lys Tyr Arg  
 10 15 20  
 15 CGC TTT CAG AGA AAC ACT GGC GAA ATG TCA TCA AAT TCA ACT GCT CTT 211  
 Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu  
 25 30 35  
 GCA CTA GTG AGA CCC TCT TCT TCT GGG TTA ATT AAC AGC AAT ACA GAC 259  
 Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp  
 20 40 45 50  
 AAC AAT CTT GCA GTC TAC GAC CTC TCT CGG GAT ATT TTA AAT AAT TTC 307  
 Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe  
 55 60 65 70  
 CCA CAC TCA ATA GCC AGG CAG AAG CGA ATA TTG GTA AAC CTC AGT ATG 355  
 25 Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met  
 75 80 85  
 GTG GAA AAC AAG CTG GTT GAA CTG GAA CAT ACT CTA CTT AGC AAG GGT 403  
 Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly  
 90 95 100  
 30 TTC AGA GGT GCA TCA CCT CAC CGG AAA TCC ACC TAAAAGCGTA CAGG 450  
 Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr  
 105 110  
 ATGTAATGCC AGTGGTGGA ATCATTAAAG ACACTTTGA GTAG 493

35

## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2044



(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Epidermoid carcinoma  
 (C) CELL LINE: KB  
 (D) CLONE NAME: HP10428

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(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 288..1385  
 (C) CHARACTERIZATION METHOD: E

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

	AGATTCCGGC CTGGAGCTCC CAGGGCCGAG CAGACCTTGG GACCTGTGAG CGCTGCATCC	60
20	AATTAACCAT GGGAAGGGTC AGCACCAGCC ACCAGCCCCT TAGGTGAGGA CTCTGCCTGG	120
	GGCTCTGCTG ATGGTTCCGA ATCATGGAGC TGCAGAGAGC TCCTCCAGCC TGGAGACGTT	180
	CTTGGTGAAA GCTGTGGTCT AACTCCACCG GCTCTTCCTG CACATTGTAT TCAAGAGGGG	240
	TGCCTGCCCC CGCTGACTCA GGAGCTCCGG TGCTGCAGCC GCCACGA ATG GGG AGG	296
		Met Gly Arg
25		1
	TGG GCC CTC GAT GTG GCC TTT TTG TGG AAG GCG GTG TTG ACC CTG GGG	344
	Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu Thr Leu Gly	
	5 10 15	
	CTG GTG CTT CTC TAC TAC TGC TTC TCC ATC GGC ATC ACC TTC TAC AAC	392
30	Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr Phe Tyr Asn	
	20 25 30 35	
	AAG TGG CTG ACA AAG AGC TTC CAT TTC CCC CTC TTC ATG ACG ATG CTG	440
	Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met Thr Met Leu	
	40 45 50	
35	CAC CTG GCC GTG ATC TTC CTC TTC TCC GCC CTG TCC AGG GCG CTG GTT	488
	His Leu Ala Val Ile Phe Leu Ph Ser Ala Leu S r Arg Ala Leu Val	
	55 60 65	
	CAG TGC TCC AGC CAC AGG GCC CGT GTG GTG CTG AGC TGG GCC GAC TAC	536

	Gln	Cys	Ser	Ser	His	Arg	Ala	Arg	Val	Val	Leu	Ser	Trp	Ala	Asp	Tyr	
			70					75					80				
	CTC	AGA	AGA	GTG	GCT	CCC	ACA	GCT	CTG	GCG	ACG	GCG	CTT	GAC	GTG	GGC	584
	Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala	Leu	Asp	Val	Gly	
5		85					90				95						
	TTG	TCC	AAC	TGG	AGC	TTC	CTG	TAT	GTC	ACC	GTC	TCG	CTG	TAC	ACA	ATG	632
	Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser	Leu	Tyr	Thr	Met	
	100					105					110					115	
	ACC	AAA	TCC	TCA	GCT	GTC	CTC	TTC	ATC	TTG	ATC	TTC	TCT	CTG	ATC	TTC	680
10	Thr	Lys	Ser	Ser	Ala	Val	Leu	Phe	Ile	Leu	Ile	Phe	Ser	Leu	Ile	Phe	
					120					125					130		
	AAG	CTG	GAG	GAG	CTG	CGC	GCG	GCA	CTG	GTC	CTG	GTG	GTC	CTC	CTC	ATC	728
	Lys	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Val	Leu	Val	Val	Leu	Leu	Ile	
					135				140					145			
15	GCC	GGG	GGT	CTC	TTC	ATG	TTC	ACC	TAC	AAG	TCC	ACA	CAG	TTC	AAC	GTG	776
	Ala	Gly	Gly	Leu	Phe	Met	Phe	Thr	Tyr	Lys	Ser	Thr	Gln	Phe	Asn	Val	
					150				155					160			
	GAG	GGC	TTC	GCC	TTG	GTG	CTG	GGG	GCC	TCG	TTC	ATC	GGT	GGC	ATT	CGC	824
	Glu	Gly	Phe	Ala	Leu	Val	Leu	Gly	Ala	Ser	Phe	Ile	Gly	Gly	Ile	Arg	
20		165					170				175						
	TGG	ACC	CTC	ACC	CAG	ATG	CTC	CTG	CAG	AAG	GCT	GAA	CTC	GGC	CTC	CAG	872
	Trp	Thr	Leu	Thr	Gln	Met	Leu	Leu	Gln	Lys	Ala	Glu	Leu	Gly	Leu	Gln	
	180					185					190					195	
	AAT	CCC	ATC	GAC	ACC	ATG	TTC	CAC	CTG	CAG	CCA	CTC	ATG	TTC	CTG	GGG	920
25	Asn	Pro	Ile	Asp	Thr	Met	Phe	His	Leu	Gln	Pro	Leu	Met	Phe	Leu	Gly	
					200					205					210		
	CTC	TTC	CCT	CTC	TTT	GCT	GTA	TTT	GAA	GGT	CTC	CAT	TTG	TCC	ACA	TCT	968
	Leu	Phe	Pro	Leu	Phe	Ala	Val	Phe	Glu	Gly	Leu	His	Leu	Ser	Thr	Ser	
					215				220					225			
30	GAG	AAA	ATC	TTC	CGT	TTC	CAG	GAC	ACA	GGG	CTG	CTC	CTG	CGG	GTA	CTT	1016
	Glu	Lys	Ile	Phe	Arg	Phe	Gln	Asp	Thr	Gly	Leu	Leu	Leu	Arg	Val	Leu	
					230				235					240			
	GGG	AGC	CTC	TTC	CTT	GGC	GGG	ATT	CTC	GCC	TTT	GGT	TTG	GGC	TTC	TCT	1064
	Gly	Ser	Leu	Phe	Leu	Gly	Gly	Ile	Leu	Ala	Phe	Gly	Leu	Gly	Phe	Ser	
35		245					250				255						
	GAG	TTC	CTC	CTG	GTC	TCC	AGA	ACC	TCC	AGC	CTC	ACT	CTC	TCC	ATT	GCC	1112
	Glu	Phe	Leu	Leu	Val	Ser	Arg	Thr	Ser	Ser	Leu	Thr	Leu	Ser	Il	Ala	
	260					265					270					275	

	GGC ATT TTT AAG GAA GTC TGC ACT TTG CTG TTG GCA GCT CAT CTG CTG	1160
	Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala His Leu Leu	
	280 285 290	
	GGC GAT CAG ATC AGC CTC CTG AAC TGG CTG GGC TTC GCC CTC TGC CTC	1208
5	Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala Leu Cys Leu	
	295 300 305	
	TCG GGA ATA TCC CTC CAC GTT GCC CTC AAA GCC CTG CAT TCC AGA GGT	1256
	Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His Ser Arg Gly	
	310 315 320	
10	GAT GGT GGC CCC AAG GCC TTG AAG GGG CTG GGC TCC AGC CCC GAC CTG	1304
	Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser Pro Asp Leu	
	325 330 335	
	GAG CTG CTG CTC CGG AGC AGC CAG CGG GAG GAA GGT GAC AAT GAG GAG	1352
	Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp Asn Glu Glu	
15	340 345 350 355	
	GAG GAG TAC TTT GTG GCC CAG GGG CAG CAG TGACCAGCCA GGGCAAAT	1400
	Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln	
	360 365	
	GGCTTAGAAG CAGGCCACTC CCCAGCCTGC TGCCAGCACT CACTGTGCTC AAGCCGCCAG	1460
20	GGCTCATCAT GGTAGCTGGG AGCTGTGGAC GGGAGTCACC AGGTGGTGGG GCCAAGCCAG	1520
	GGACTCATGA CTTTTGCCCC TCCCTTCAGA GCCTGGTCAC ACAAGGGGCG AGCACCAGGC	1580
	CAGCCTGGGA CTGGCCAGAG CTGGGCCCAA GCTGCGCTGG AATCGCAGCA GGAGAGGGGA	1640
	GTGGGCTGGT TCTTCCCACC ACTTCCCAGG CTCTGACAGC CGAGACTCAT TTCCAAGGCA	1700
	CAGCAGCTTT CTAAAGGGAC TGAGTTTGGG CTGGGTTTTG GACCTCCAGG GGCTGGAGCT	1760
25	TCATCACCTG GGCAGTGTCT TTTCTCAGAG AGCAGGTTTC TTTATAGTTT GGAAATAAAT	1820
	GGTTACGGT CCACTGGCCG CCTTGTTGTTG CTGGAGACGT GGGGGCAGGG AGGGGACAGT	1880
	GTGGGCCTGG CCTCTCCTTT CCTTCCCTG CCTGGAGCCT TCTTCAAATG TCTGGTCTTA	1940
	AGCCAGGCCT CCTTCATTTT CTCGCTCCTG TTAGAACACC AGTCCCCTCC CCAGTGGGGC	2000
	CCCACTGCAC CTGCTGGCAG GAAATAAATG AATGTTTACT GAGT	2044
30		

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043

35 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10429

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## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 157.. 837  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

	ATTAGCATAA CCCTTCCTCA GGAAGAGTGA GATTTTATAT TTGACAATAA AGTGTTAGAC	60
	TCCATTCTA AATACCAGAC TTCAAAAGAT AAGGTTCAAA AGTGTTATAA GAAGATATTC	120
15	CTTTTTTGT CCTAGAGAAC TTATTTCTCT GTGAAA ATG CCT ACC ACA AAG AAG	174
	Met Pro Thr Thr Lys Lys	
	1 5	
	ACA TTG ATG TTC TTA TCA AGC TTT TTC ACC AGC CTT GGG TCC TTC ATT	222
	Thr Leu Met Phe Leu Ser Ser Phe Phe Thr Ser Leu Gly Ser Phe Ile	
20	10 15 20	
	GTA ATT TGC TCT ATT CTT GGG ACA CAA GCA TGG ATC ACC AGT ACA ATT	270
	Val Ile Cys Ser Ile Leu Gly Thr Gln Ala Trp Ile Thr Ser Thr Ile	
	25 30 35	
	GCT GTT AGA GAC TCT GCT TCA AAT GGG AGC ATT TTC ATC ACT TAC GGA	318
25	Ala Val Arg Asp Ser Ala Ser Asn Gly Ser Ile Phe Ile Thr Tyr Gly	
	40 45 50	
	CTT TTT CGT GGG GAG AGT AGT GAA GAA TTG AGT CAC GGA CTT GCA GAA	366
	Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu Ser His Gly Leu Ala Glu	
	55 60 65 70	
30	CCA AAG AAA AAG TTT GCA GTT TTA GAG ATA CTG AAT AAT TCT TCC CAA	414
	Pro Lys Lys Lys Phe Ala Val Leu Glu Ile Leu Asn Asn Ser Ser Gln	
	75 80 85	
	AAA ACT CTG CAT TCG GTG ACT ATC CTG TTC CTG GTC CTG AGT TTG ATC	462
	Lys Thr Leu His Ser Val Thr Ile Leu Phe Leu Val Leu Ser Leu Ile	
35	90 95 100	
	ACG TCG CTG CTG AGC TCT GGG TTT ACC TTC TAC AAC AGC ATC AGC AAC	510
	Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe Tyr Asn Ser Ile Ser Asn	
	105 110 115	

	CCT TAC CAG ACA TTC CTG GGG CCG ACG GGG GTG TAC ACC TGG AAC GGG	558
	Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly Val Tyr Thr Trp Asn Gly	
	120 125 130	
	CTC GGT GCA TCC TTC GTT TTT GTG ACC ATG ATA CTG TTT GTG GCG AAC	606
5	Leu Gly Ala Ser Phe Val Phe Val Thr Met Ile Leu Phe Val Ala Asn	
	135 140 145 150	
	ACG CAG TCC AAC CAA CTC TCC GAA GAG TTG TTC CAA ATG CTT TAC CCG	654
	Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu Phe Gln Met Leu Tyr Pro	
	155 160 165	
10	GCA ACC ACC AGT AAA GGA ACG ACC CAC AGT TAC GGA TAC TCG TTC TGG	702
	Ala Thr Thr Ser Lys Gly Thr Thr His Ser Tyr Gly Tyr Ser Phe Trp	
	170 175 180	
	CTC ATA CTG CTC GTC ATT CTT CTA AAT ATA GTC ACT GTA ACC ATC ATC	750
	Leu Ile Leu Leu Val Ile Leu Leu Asn Ile Val Thr Val Thr Ile Ile	
15	185 190 195	
	ATT TTC TAC CAG AAG GCC AGA TAC CAG CGG AAG CAG GAG CAG AGA AAG	798
	Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg Lys Gln Glu Gln Arg Lys	
	200 205 210	
	CCA ATG GAA TAT GCT CCA AGG GAC GGA ATT TTA TTC TGAATTCTCT TTCATC	850
20	Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile Leu Phe	
	215 220 225	
	TCATTTTGGC GTTGCACTA TTGTACATCA GCCCTGAGTA GTAAGTGGTT AGCTTCTCTG	910
	GACAATTCAG CATGGTAACG TGAAGTGCAT CTGTGACAGC ATTTGTGTTT CATGACACTG	970
	TGTTCTTCAT TGATGCTGTA CTCCTGAAAA TTTTCCAC AAGGTTGGGG AAATGAATGG	1030
25	GAAATGTCGC TGG	1043

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 972  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 5 (B) EXISTENCE POSITION: 29.. 418  
 (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

10 AGACAGCGGC GGGCGCAGGA CGTGCACT ATG GCT CGG GGC TCG CTG CGC CGG      52
                                     Met Ala Arg Gly Ser Leu Arg Arg
                                     1           5
    TTG CTG CGG CTC CTC GTG CTG GGG CTC TGG CTG GCG TTG CTG CGC TCC      100
    Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
15      10           15           20
    GTG GCC GGG GAG CAA GCG CCA GGC ACC GCC CCC TGC TCC CGC GGC AGC      148
    Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
      25           30           35           40
    TCC TGG AGC GCG GAC CTG GAC AAG TGC ATG GAC TGC GCG TCT TGC AGG      196
20 Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
      45           50           55
    GCG CGA CCG CAC AGC GAC TTC TGC CTG GGC TGC GCT GCA GCA CCT CCT      244
    Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
      60           65           70
25 GCC CCC TTC CGG CTG CTT TGG CCC ATC CTT GGG GGC GCT CTG AGC CTG      292
    Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
      75           80           85
    ACC TTC GTG CTG GGG CTG CTT TCT GGC TTT TTG GTC TGG AGA CGA TGC      340
    Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
30      90           95           100
    CGC AGG AGA GAG AAG TTC ACC ACC CCC ATA GAG GAG ACC GGC GGA GAG      388
    Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
    105           110           115           120
    GGC TGC CCA GCT GTG GCG CTG ATC CAG TGACA ATGT GCCCCCTGCC A CCGG      440
35 Gly Cys Pro Ala Val Ala Leu Ile Gln
      125
    GGCTCGCCCA CTCATCATTC ATTATCCAT TCTAGAGCCA GTCTCTGCCT CCCAGACGCG      500
    CGGGGAGCCA AGCTCCTCCA ACCACAAGGG GGGTGGGGGG CGGTGAATCA CCTCTGAGGC      560

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CTGGGCCCAG GGTTCAGGGG AACCTTCCAA GGTGTCTGGT TGCCCTGCCT CTGGCTCCAG 620
AACAGAAAGG GAGCCTCACG CTGGCTCACA CAAAACAGCT GACACTGACT AAGGAACTGC 680
AGCATTTCGA CAGGGGAGGG GGGTGCCCTC CTTCTAGAG GCCCTGGGGG CCAGGCTGAC 740
TTGGGGGGCA GACTTGACAC TAGGCCCCAC TCACTCAGAT GTCCTGAAAT TCCACCACGG 800
5 GGGTCACCCT GGGGGGTTAG GGACCTATTT TTAACACTAG GGGGCTGGCC CACTAGGAGG 860
GCTGGCCCTA AGATACAGAC CCCCCCACT CCCCAAAGCG GGGAGGAGAT ATTTATTTTG 920
GGGAGAGTTT GGAGGGGAGG GAGAATTTAT TAATAAAGA ATCTTAACT TT 972

```

10 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- 20 (B) CELL KIND: Liver
- (C) CELL LINE:
- (D) CLONE NAME: HP10433

(ix) SEQUENCE CHARACTERISTICS:

- 25 (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 73.. 564
- (C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

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30 AAGATTTTCAG CTGCGGGACG GTCAGGGGAG ACCTCCAGGC GCAGGGAAGG ACGGCCAGGG 60
TGACACGGAA GC ATG CGA CGG CTG CTG ATC CCT CTG GCC CTG TGG CTG GGC 111
      Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
          1             5             10
35 GCG GTG GGC GTG GGC GTC GCC GAG CTC ACG GAA GCC CAG CGC CGG GGC 159
Ala Val Gly Val Gly Val Ala Glu L u Thr Glu Ala Gln Arg Arg Gly
      15             20             25
CTG CAG GTG GCC CTG GAG GAA TTT CAC AAG CAC CCG CCC GTG CAG TGG 207

```

	Leu	Gln	Val	Ala	Leu	Glu	Glu	Phe	His	Lys	His	Pro	Pro	Val	Gln	Trp	
	30				35					40					45		
	GCC	TTC	CAG	GAG	ACC	AGT	GTG	GAG	AGC	GCC	GTG	GAC	ACG	CCC	TTC	CCA	255
	Ala	Phe	Gln	Glu	Thr	Ser	Val	Glu	Ser	Ala	Val	Asp	Thr	Pro	Phe	Pro	
5					50					55					60		
	GCT	GGA	ATA	TTT	GTG	AGG	CTG	GAA	TTT	AAG	CTG	CAG	CAG	ACA	AGC	TGC	303
	Ala	Gly	Ile	Phe	Val	Arg	Leu	Glu	Phe	Lys	Leu	Gln	Gln	Thr	Ser	Cys	
					65					70					75		
	CGG	AAG	AGG	GAC	TGG	AAG	AAA	CCC	GAG	TGC	AAA	GTC	AGG	CCC	AAT	GGG	351
10	Arg	Lys	Arg	Asp	Trp	Lys	Lys	Pro	Glu	Cys	Lys	Val	Arg	Pro	Asn	Gly	
					80					85					90		
	AGG	AAA	CGG	AAA	TGC	CTG	GCC	TGC	ATC	AAA	CTG	GGC	TCT	GAG	GAC	AAA	399
	Arg	Lys	Arg	Lys	Cys	Leu	Ala	Cys	Ile	Lys	Leu	Gly	Ser	Glu	Asp	Lys	
					95					100					105		
15	GTT	CTG	GGC	CGG	TTG	GTC	CAC	TGC	CCC	ATA	GAG	ACC	CAA	GTT	CTG	CGG	447
	Val	Leu	Gly	Arg	Leu	Val	His	Cys	Pro	Ile	Glu	Thr	Gln	Val	Leu	Arg	
					110					115					120	125	
	GAG	GCT	GAG	GAG	CAC	CAG	GAG	ACC	CAG	TGC	CTC	AGG	GTG	CAG	CGG	GCT	495
	Glu	Ala	Glu	Glu	His	Gln	Glu	Thr	Gln	Cys	Leu	Arg	Val	Gln	Arg	Ala	
20					130					135					140		
	GGT	GAG	GAC	CCC	CAC	AGC	TTC	TAC	TTC	CCT	GGA	CAG	TTC	GCC	TTC	TCC	543
	Gly	Glu	Asp	Pro	His	Ser	Phe	Tyr	Phe	Pro	Gly	Gln	Phe	Ala	Phe	Ser	
					145					150					155		
	AAG	GCC	CTG	CCC	CGC	AGC	TAAGCCAGCA	CTGAGCTGCG	TGGTGCCTC								
25	Lys	Ala	Leu	Pro	Arg	Ser											
					160												
	CAGGACCGCT	GCCGGTGGTA	ACCACTGGAA	GACCCCAGCC	CCCAGGGAGA	GGACCCCGTT	650										
	CTATCCCCAG	CCATGATAAT	AAAGCTGCTC	TCCCAGCTGC	CTCTC		695										

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1914

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10480

5

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 80.. 661  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

	ACTCTCTGCT GTCGCCCGTC CCGCGCGCTC CTCCGACCCG CTCCGCTCCG CTCCGCTCGG	60
	CCCCGCGCCG CCGTCAAC ATG ATC CGC TGC GGC CTG GCC TGC GAG CGC TGC	112
15	Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys	
	1 5 10	
	CGC TGG ATC CTG CCC CTG CTC CTA CTC AGC GCC ATC GCC TTC GAC ATC	160
	Arg Trp Ile Leu Pro Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile	
	15 20 25	
20	ATC GCG CTG GCC GGC CGC GGC TGG TTG CAG TCT AGC GAC CAC GGC CAG	208
	Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln	
	30 35 40	
	ACG TCC TCG CTG TGG TGG AAA TGC TCC CAA GAG GGC GGC GGC AGC GGG	256
	Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly	
25	45 50 55	
	TCC TAC GAG GAG GGC TGT CAG AGC CTC ATG GAG TAC GCG TGG GGT AGA	304
	Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg	
	60 65 70 75	
	GCA GCG GCT GCC ATG CTC TTC TGT GGC TTC ATC ATC CTG GTG ATC TGT	352
30	Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys	
	80 85 90	
	TTC ATC CTC TCC TTC TTC GCC CTC TGT GGA CCC CAG ATG CTT GTC TTC	400
	Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe	
	95 100 105	
35	CTG AGA GTG ATT GGA GGT CTC CTT GCC TTG GCT GCT GTG TTC CAG ATC	448
	Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile	
	110 115 120	
	ATC TCC CTG GTA ATT TAC CCC GTG AAG TAC ACC CAG ACC TTC ACC CTT	496

	Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu	
	125 130 135	
	CAT GCC AAC CGT GCT GTC ACT TAC ATC TAT AAC TGG GCC TAC GGC TTT	544
	His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe	
5	140 145 150 155	
	GGG TGG GCA GCC ACG ATT ATC CTG ATC GGC TGT GCC TTC TTC TTC TGC	592
	Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys	
	160 165 170	
	TGC CTC CCC AAC TAC GAA GAT GAC CTT CTG GGC AAT GCC AAG CCC AGG	640
10	Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg	
	175 180 185	
	TAC TTC TAC ACA TCT GCC TA ACTTGGG AATGAATGTG GGAGAAAATC GCT	690
	Tyr Phe Tyr Thr Ser Ala	
	190	
15	GCTGCTGAGA TGGACTCCAG AAGAAGAAAC TGTTTCTCCA GGCGACTTTG AACCCATTTT	750
	TTGGCAGTGT TCATATTATT AAAC TAGTCA AAAATGCTAA AATAATTTGG GAGAAAATAT	810
	TTTTTAAGTA GTGTTATAGT TTCATGTTTA TCTTTTATTA TGTTTTGTGA AGTTGTGTCT	870
	TTTCACTAAT TACCTATACT ATGCCAATAT TTCCTTATAT CTATCCATAA CATTTATACT	930
	ACATTTGTAA GAGAATATGC ACGTGAAACT TAACACTTTA TAAGGTAAAA ATGAGGTTTC	990
20	CAAGATTTAA TAATCTGATC AAGTTCTTGT TATTTCCAAA TAGAATGGAC TTGGTCTGTT	1050
	AAGGGCTAAG GAGAAGAGGA AGATAAGGTT AAAAGTTGTT AATGACCAAA CATTCTAAAA	1110
	GAAATGCAAA AAAAAAGTTT ATTTTCAAGC CTTCGAACTA TTTAAGGAAA GCAAAATCAT	1170
	TTCTAAATG CATATCATTT GTGAGAAATT CTCATTAATA TCCTGAATCA TTCATTTGAG	1230
	CTAAGGCTTC ATGTTGACTC GATATGTCAT CTAGGAAAGT ACTATTTTCAT GGTCCAAACC	1290
25	TGTTGCCATA GTTGGTAAGG CTTTCCTTTA AGTGTGAAAT ATTTAGATGA AATTTTCTCT	1350
	TTTAAAGTTC TTTATAGGGT TAGGGTGTGG GAAAATGCTA TATTAATAAA TCTGTAGTGT	1410
	TTTGTGTTTA TATGTTTACA ACCAGAGTAG ACTGGATTGA AAGATGGACT GGGTCTAATT	1470
	TATCATGACT GATAGATCTG GTTAAGTTGT GTAGTAAAGC ATTAGGAGGG TCATTCTTGT	1530
	CACAAAAGTG CCACTAAAAC AGCCTCAGGA GAATAAATGA CTTGCTTTTC TAAATCTCAG	1590
30	GTTTATCTGG GCTCTATCAT ATAGACAGGC TTCTGATAGT TTGCAACTGT AAGCAGAAAC	1650
	CTACATATAG TTAATAATCCT GGTCTTTCTT GGTAAACAGA TTTTAAATGT CTGATATAAA	1710
	ACATGCCACA GGAGAATTCG GGGATTTGAG TTTCTCTGAA TAGCATATAT ATGATGCATC	1770
	GGATAGGTCA TTATGATTTT TTACCATTTT GACTTACATA ATGAAAACCA ATTCATTTTA	1830
	AATATCAGAT TATTATTTTG TAAGTTGTGG AAAAAGCTAA TTGTAGTTTT CATTATGAAG	1890
35	TTTCCCAAT AAACCAGGTA TTCT	1914